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Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

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TYPE OF SEARCH:
NA Sequences: _____
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VENDOR/COST (where applic.)
STN: _____
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Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

STIC CM 1000 2000
Technical Information Series
RHP 01000
RHP 01000

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Db 2319 TATCTCATATTTGCTAGTATGATTTTACAAAGCTGAGCGCTTGAATATGAGTAAAT 2378

QY	2283	AAAGTCTGTCCCTTTAAACCTTTCGTTTGCACTGCATTTGATTTCCACTCAATGTT	2442
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QY	2443	GGCAAACTTTCCGAAGAGATCTACTGAGTCTTGCAAGAAAGGTTACTACAGTACCCAT	2502
Db	2439	GGCAAGCTCTCTGGAGAGATATCTGACCTCTGCAGAGATGTATCCGACAGTCCGCT	2498
QY	2503	GTGTTTCAAAACCTGTTAGAAATGCTGAGTGTGTTTCACGTTCCACTCACCTTACAGAGATG	2562
Db	2499	GTGTTTTCAAAGCTGGTAACCATGCTTAATGCTTGCGCTCCACCATTTACACAGATG	2558
QY	2563	CGTCCCGCTTTGATGCGCTATTCGACATGTAGAGTGAATTTCCGAAGCATCCAGTTGGC	2622
Db	2559	CGCGCGGCTGTGATGCTATCGGGGATGTAGTAATTTGCCGAGTGCATCCAGTGGGT	2618
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QY	2683	TATCTGGAAACACAGAGAACACTTCCCTGAGTGCACAGTCCATTTAGAAAACTGA	2742
Db	2676	TGTCCT-----AGAAAACACTCCCTTTGAGCACAGTGCATAGAGAGAAAACTGGA	2726
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Db	3534	ATGGGATGTACAGGTGTCTCAGGATGGCCCTCCCATGTCTCCCTACGCTCAGGTTGMAAT	3593
OY	3643	GGAGAGATATCATCTATTATTCACAGGATPACACAGACCTCTACAGCAATACCAA	3702
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OY	4483	CCTAGAGCAACCTGCATCAAGAGAGCTACGAACATCTCAGTCTTCTGTACTATACATGG	4542
Db	4434	CCTAGAGCAAGGCTCTCGTCCAGAGAGAGCTGTAAACAATCTCGGTCTTCCGACCGTGG	4493
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RESULT 2

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US-10-000-864-7
; Sequence 7, Application US/10000864
; Patent No. US20020146798A1
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
; FILE REFERENCE: CPT-085CPC
; CURRENT APPLICATION NUMBER: US/10/000,864
; EARLIER FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: USSN 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: USSN 60/099,165
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5253
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(4493)
US-10-000-864-7
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Query Match 65.1% Score 3417; Db 12; Length 5253;
Best Local Similarity 83.5% Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;
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Db 3894 AGGTGTGAGAGAGATATGATGATGATGATGATGATGATGATGATGATGATG 3953
QY 4003 CATTTGTGAGTAAATATGAGAGCTTCAAGAGATGATGATGATGATGATGATG 4062
Db 3954 CACCTCTGAGTAAATATGAGAGCTTCAAGAGATGATGATGATGATGATGATG 4013
QY 4063 TTACCTCCCTGCTTCTGATATCTCATGATAAACCATATTCACAGAGATGATG 4122
Db 4014 TTACCTCCCTGCTTCTGATATCTCATGATAAACCATATTCACAGAGATGATG 4073
QY 4123 GCCAATTTGCTAATATGAGAGCTGTCAGAGATGATGATGATGATGATGATG 4182
Db 4074 GCCAATTTGCTAATATGAGAGCTGTCAGAGATGATGATGATGATGATGATG 4133
QY 4183 GCCAGTTGGATCAAAAGAGATGTCAGAGATGTCAGAGATGTCAGAGATGTC 4242
Db 4134 GCCAGTTGGATCAAAAGAGATGTCAGAGATGTCAGAGATGTCAGAGATGTC 4193
QY 4243 ATTGATTTATGAGAGCTGAGAGTACTAAGAGTCAACAGTATGAGAGAGTGTATG 4302
Db 4194 ATTGATTTATGAGAGCTGAGAGTACTAAGAGTCAACAGTATGAGAGAGTGTATG 4253
QY 4303 TGGAGTTGGTGTGATTAATAGAAATGGCTTGCAGAAACCAATGGAATGAGAA 4362
Db 4254 TGGAGTTGGTGTGATTAATAGAAATGGCTTGCAGAAACCAATGGAATGAGAA 4313
QY 4363 AAACATCAATCATCTTGTGATTTAAGATTTAGATGCTAGTCAACTGCTCATG 4422
Db 4314 AAACATCAATCATCTGCTGATTTAAGATTTAGATGCTAGTCAACTGCTCATG 4373
QY 4423 ATCCCTTACATTTGTCTCTGCTTACAGATGCTGCTCTGCTGCTTACATTTCA 4482
Db 4374 ATCCCTTACATTTGTCTCTGCTTACAGATGCTGCTCTGCTGCTTACATTTCA 4433
QY 4483 CCTCAGAGAGAGCTCCTCAGAGAGAGTACTAGAGAGAGTCTGCTTCACTCATG 4542
Db 4434 CCTCAGAGAGAGCTCCTCAGAGAGAGTACTAGAGAGAGTCTGCTTCACTCATG 4493
QY 4543 TAGCCATTTATGAGAGAGTACTAGTAAAGAGAGATGCTCAAGAGAGAGAGAG 4602
Db 4494 TAGCCATTTATGAGAGAGTACTAGTAAAGAGAGATGCTCAAGAGAGAGAGAG 4553

QY 4603 TG-----TGGGGAACCAATGATTAATTTACTGCGCATGATGCCACTGAACGCTTGAAC 4658
Db 4554 AGAACTTGTGGGCAACATGCGCTTAACCGGACCGCTCAGCGCACTGAACACCGAAGAAC 4613
QY 4659 GAGGCGAGTGGGGAACCGTTACTAGTATGATGATGATGATGATGATGATGATGATG 4718
Db 4614 GGGGCGAGGCGGGA-CCGTACCTTAAGATGATGATGATGATGATGATGATGATGATG 4672
QY 4719 CTCAGTATGCA-AAAGCCCAAACTAGTGCAGAACTGTAAGTGTGCTTCAAGAACT 4777
Db 4673 CTCAGTATGCAACATCTACCTGCTGAGAGAGTGCAGACCTGCTTACAGAGACT 4732
QY 4778 GCGCTAGTGTGAACAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 4837
Db 4733 GCGCTGAGGAGACAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 4792
QY 4838 TATTTTGTGAGCACTTTTCAGCAA 4864
Db 4793 TA-TTTTGTGAGCACTTTTCAGCTA 4817

RESULT 3
US-10-000-864-1
Sequence 1, Application US/10000864
Patent No. US20020146798A1
GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEK1 PROTEIN AND NUCLEIC ACID MOLECULES
FILE REFERENCE: CPT-085CPC
CURRENT APPLICATION NUMBER: US/10/000,864
CURRENT FILING DATE: 2001-10-31
EARLIER APPLICATION NUMBER: 09/423,890
EARLIER FILING DATE: 2000-06-03
EARLIER APPLICATION NUMBER: PCT/US99/05556
EARLIER FILING DATE: 1999-03-15
EARLIER APPLICATION NUMBER: USSN 60/078,153
EARLIER FILING DATE: 1998-03-16
EARLIER APPLICATION NUMBER: USSN 60/099,165
EARLIER FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3911
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(3908)
US-10-000-864-1

Query Match 62.7%; Score 3286.4; DB 12; Length 3911.
Best Local Similarity 90.5%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

QY 590 CAGCTGGAAGCAGATGTTGGAAGAGAAATAGCGAGGCTGTGTGTAATAC 649
Db 1 CGGCTGGAAGCAGATGTTGGAAGAGAAATAGCGAGGCTGTGTGTAATAC 60
QY 650 CAATCCGATTAAAGAGATGATGTAATTAATCACTTACACTAGTGTCCAGAG 709
Db 61 CAATCCGATTAAAGAGATGATGTAATTAATCACTTACACTAGTGTCCAGAG 120
QY 710 AGTCCAGAGAGTGGGCTTACAGAGTTCGAAAGGCGAGAGTCTCTCTGGA 769
Db 121 AGTCCAGAGAGTGGGCTTACAGAGTTCGAAAGGCGAGAGTCTCTCTGGA 180
QY 770 ACTCCCATCAGTGCAGAGTGAATGAGATTCAGAGAGTAAAGAGAGAGATT 829
Db 181 ACTCCCATCAGTGCAGAGTGAATGAGATTCAGAGAGTAAAGAGAGAGATT 240
QY 830 CCCAGTGCCTTTTACAGAGTGCAGATCACACCCCGAGAGAGCTTCCAGATG 889

Db 241 CCCCAGTCCCTTTTCAGAGTGGCAATCAACACCACCCGAAAGCCCTTCCACCAATG 300
QY 890 GCTTCTACCAATATATAGCCCTGAGGAAACAAACCGCGTGTATTAACAAAGTATCGGGCCA 949
Db 301 GCTTCTACCAATATATAGCCCTGAGGAAACAAACCGCGTGTATTAACAAAGTATCGGGCCA 360
QY 950 GACTGTACTTACTGACAGATAGGGCCCTAACTCTTCTGATTTGAGAGACAGCCAG 1009
Db 361 GACTGTACTTACTGACAGATAGGGCCCTAACTCTTCTGATTTGAGAGACAGCCAG 420
QY 1010 ACAATAAATACCGGCTTTATTTGGGCTTCAGACATGCGACCTGTGAAACATTTCT 1069
Db 421 ACAATAAATACCGGCTTTATTTGGGCTTCAGACATGCGACCTGTGAAACATTTCT 480
QY 1070 GATTCATCTGCTATTTGTGATGCTCCGGGCTTTCACTAGAACCTTGCAGACCAATGT 1129
Db 481 GATTCATCTGCTATTTGTGATGCTCCGGGCTTTCACTAGAACCTTGCAGACCAATGT 540
QY 1130 TATGAGAAAAAATTTTAAAGAAATTTTGAAGTTGAGAGATTTGTTCCAGAAATATCACAGTA 1189
Db 541 TATGAGAAAAAATTTTAAAGAAATTTTGAAGTTGAGAGATTTGTTCCAGAAATATCACAGTA 600
QY 1190 GGGTAGCTCAAGATCAAAAGCTCCATCTGCTAACACATCCAGAAAGTTGTTTCAGCA 1249
Db 601 GGGTAGCTCAAGATCAAAAGCTCCATCTGCTAACACATCCAGAAAGTTGTTTCAGCA 660
QY 1250 TGTCAATTTCTCATATCTGTCATCATCTAGTACTTCTACGTTAGTTGAGAAACGCA 1309
Db 661 TGTCAATTTCTCATATCTGTCATCATCTAGTACTTCTACGTTAGTTGAGAAACGCA 720
QY 1310 TAAAGATGAGAGAAACAGATGTCTTAATTTGCTTTGGGCAATGCTGATGAAGAA 1369
Db 721 TAAAGATGAGAGAAACAGATGTCTTAATTTGCTTTGGGCAATGCTGATGAAGAA 780
QY 1370 GCTTACAGTGTGTGAAGAGGCTGCAGAGAAAGCTGCACCACTGATGATGCAATTT 1429
Db 781 GCTTACAGTGTGTGAAGAGGCTGCAGAGAAAGCTGCACCACTGATGATGCAATTT 840
QY 1430 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCTAATG 1489
Db 841 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCTAATG 900
QY 1490 GGAATCTCATGATTTTCTACAGCCAGATGTTCGAAGTCTGTGATTTCCCTTTCTCC 1549
Db 901 GGAATCTCATGATTTTCTACAGCCAGATGTTCGAAGTCTGTGATTTCCCTTTCTCC 960
QY 1550 TCAGAGCTGCACAGCAAAACGCTACAGAGAGAGCTTTGGCTGATCAAGAAATC 1609
Db 961 TCAGAGCTGCACAGCAAAACGCTACAGAGAGAGCTTTGGCTGATCAAGAAATC 1020
QY 1610 AAGAGAGCAATTTTAACTTACTCATTTATGAACTCAGCAAAATCCCTCCGCTTACAAAG 1669
Db 1021 AAGAGAGCAATTTTAACTTACTCATTTATGAACTCAGCAAAATCCCTCCGCTTACAAAG 1080
QY 1670 ATTATGCTGAGCCATGATTCAGGTGTGGAATGGAATCGTTGGCTGCTAATTTCTA 1729
Db 1081 ATTATGCTGAGCCATGATTCAGGTGTGGAATGGAATCGTTGGCTGCTAATTTCTA 1140
QY 1730 GAAACTGGAATGTGAGAGATGGCCCTCAGGGCTTTTCCCATGATGTAGTGGGGCC 1789
Db 1141 GAAACTGGAATGTGAGAGATGGCCCTCAGGGCTTTTCCCATGATGTAGTGGGGCC 1200
QY 1790 TGTGTTGGCAATGGGAGAGCACTGAAATTTGTGGGGCAGACAGTGAAGAGCCGA 1849
Db 1201 TGTGTTGGCAATGGGAGAGCACTGAAATTTGTGGGGCAGACAGTGAAGAGCCGA 1260
QY 1850 GTGGGGAGCCACAGTGGGCTTCCAGACAGATCTCAGAGAGATGTGTGGAGCAT 1909
Db 1261 GTGGGGAGCCAGCGGCTCTCCAGCCAGCAATCTCAGGGAGATGTGTGGAGCGT 1320
QY 1910 GTGGAGCGTGTGTCAATGTGTGTGACCTGTCTTCAAAAGTGTAGTGTGCTT 1369
Db 1321 GTGTGAGTGTCTGTCTATGATGTGCGGTGACCCCTGTCTCAAAAGTGTAGTGTGCTT 1380
QY 1970 TAAAAACATTGAGAGCCATGCTGATATATCTCCTTCCACAGTTTGAAGAAAGATCA 2029
Db 1381 TAAAAACATTGAGAGCCATGCTGATATATCTCCTTCCACAGTGTGAGAAAGATCA 1440
QY 2030 AACTTCAGAGACTTCTCAGCCAGTTGTAGACACATCTAGTCAAAATGTGAGATGCCA 2089
Db 1441 AACTTCAGAGACTTCTCAGCCAGTTGTAGACACATCTAGTCAAAATGTGAGATGCCA 1500
QY 2090 ATAGCCGACAAAGTACAGCTGTCCATATCAACACACTGTGGAACGTGTGAAAGCCAGAC 2149
Db 1501 ACAGCCGACAAAGTACAGCTGTCCATATCTACAGTGTGGAACCTGTGAAAGCCAGAC 1560
QY 2150 GAGAGTGGAGTGGAGAGAAATACTTAAAGGTGATCATGATGATGATGATGATGATG 2209
Db 1561 GAGAGTGGAGTGGAGAGAAATACTTAAAGGTGATCATGATGATGATGATGATGATG 1620
QY 2210 ATTATGCTTAAATTTGATTTCTTGAACCAACAACTGAATCAAAATTTGCAAGACTTC 2269
Db 1621 ATTATGCTTAAATTTGATTTCTTGAACCAACAACTGAATCAAAATTTGCAAGACTTC 1680
QY 2270 TTGGCCGCTTTGTCTTATAGATGACTGTGTTGGAATTTCCGCTGAATTTATCTC 2329
Db 1681 TTGGCCGCTTTGTCTTATAGATGACTGTGTTGGAATTTCCGCTGAATTTATCTC 1740
QY 2330 ATATGTCACTAGTATGATTTCAACAACTGACAGCTGTTGAATAGATGATTAAGAGCTG 2389
Db 1741 ATATGTCACTAGTATGATTTCAACAACTGACAGCTGTTGAATAGATGATTAAGAGCTG 1800
QY 2390 TGTCCCTTTAACCTTTGCTTGAGTCAATGTAAATTCACACTCAATGTTGGCAAC 2449
Db 1801 TGTCCCTTTAACCTTTGCTTGAGTCAATGTAAATTCACACTCAATGTTGGCAAC 1860
QY 2450 TTTCAGAAAGATCTACTTATGATTTCTGCAAGAAAGTGTACTACAGTACCCATGTGTT 2509
Db 1861 TTTCAGAAAGATCTACTTATGATTTCTGCAAGAAAGTGTACTACAGTACCCATGTGTT 1920
QY 2510 CAAAACGTTTAAAGAAATGCTAGTGTTCAGATTCACACTTACAGAGATGAGTGGCC 2569
Db 1921 CAAAACGTTTAAAGAAATGCTAGTGTTCAGATTCACACTTACAGAGATGAGTGGCC 1980
QY 2570 GTTTGATGCTATTTGACAGATGAGGTGAAATTTGCCAAGCCATCAATGGGCTAGAG 2629
Db 1981 GTTTGATGCTATTTGACAGATGAGGTGAAATTTGCCAAGCCATCAATGGGCTAGAG 2040
QY 2630 ACACTTGTGATGTGCAACAGAGACAGCTTGTGAGAGATGTGTTCCCAACATATCTGG 2689
Db 2041 ACACTTGTGATGTGCAACAGAGACAGCTTGTGAGAGATGTGTTCCCAACATATCTGG 2095
QY 2690 AAACACAGAGAACAGTTCCTGAGTGCACAGTCCATTTAGAGAAACTGSAAGAGAT 2749
Db 2096 AAACACAGAGAACAGTTCCTGAGTGCACAGTCCATTTAGAGAAACTGSAAGAGAT 2148
QY 2750 TATGTGCTACAAAATTTGATGTGACAGTTCAGAGACATTTCTGAGAGATTTGAGAT 2809
Db 2149 TATGTGCTACAAAATTTGATGTGACAGTTCAGAGACATTTCTGAGAGATTTGAGAT 2268
QY 2810 CAGTAGACCTTCTAGTTCACAAACAAACACACACACACACACACACACACACAC 2869
Db 2209 CAGTAGACCTTCTAGTTCACAAACAAACACACACACACACACACACACACACAC 2253
QY 2870 TGGTTCAACAAAAGGAGACCCACAGTCAAGTGTGAACTCCTCTTATATCATC 2929
Db 2254 TGGTTCAACAAAAGGAGACCCACAGTCAAGTGTGAACTCCTCTTATATCATC ---TC 2310
QY 2930 ATTCCCAATTAATGTTTCAAGCTTGTCAACCCCTTCTTCTTACCCCATCTGTACAG 2989
Db 2311 ATGCTCAATTAATGTTTCCAGACACATCAGCCCTTGTCTCTGCCCCGCTGTGC --- 2367
QY 2990 CTGGCACTGCACAGATGTCTCTAAGATAGACTTCAGGATTCATTCCTGCAAAATAC 3049
Db 2368 CTGGCACTGCACAGATGTCTCTAAGATAGACTTCAGGATTCATTCCTGCAAAATAC 2415


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||||| 2355 ATTGCGGCGGACATCTACACCGCTCCATCCGCTCACACCTGTCCCGGGGTCTGCCGCGAC 2414
||||| 4456 GTGGCTCTTGTGTTTGAAGCTTCAAGCTCAGAGACAGCTCCATCAAGAGAGACTACTG 4515
||||| 2415 GTGGCGGTGCGGCTTAGAAGCTTCAAGCTCAGAGACCGGCTCCGTCAGAGAGAGTGTG 2474
||||| 4516 AAGCATCCAGTCTTCTGCTACTAGTGTAGCCAAATTATGACATCACTACACTAGAAAC 4575
||||| 2475 AAACATCCGGTCTTCGCTACGACGTGTAGTTAAATTGTCTACGCTATATGAGAC 2534
||||| 4576 AGGATGCTCAACAGAGAAAAAACTTG---TGGGGAACCATTTGATTTCTACTGG 4631
||||| 2535 AGGATATCCAGACCGGAGAGAGAAAAAGAACTTGTGGCGACCATTCGCGTACCGCGAC 2594
||||| 4632 CCATGATGCTGAGTGAACAGCTATGAAGAGGCCAGTGGGAAACCTTACCTAGATGTG 4691
||||| 2595 CCTCAGCGCTAGTAAGACAGCCAGAAAGGGGCGAGCGGGGAA--CGTACTTAAGCATGTG 2653
||||| 4692 ATTGCAATTCATGATCTTACTTACCTAGCTCAGTATGCA--AAAGCCAAACTAGTCAGAA 4750
||||| 2654 ATTGCAAAATTCATGATCTTACTTACCTAGCTCAGTATGCAACATCTACCTGTCAGAGA 2713
||||| 4751 ACTGTAACCTGTGCTTTCGAAGAACTGCGCTAGTGAAGAGAAACAAATGAACTTGG 4810
||||| 2714 ACTGCACACCGGTCTTTCACAGAGACTGCTGCGGGGACAGGAAGCGGATGGAGTTTG 2773
||||| 4811 CATGACTAATTCAGAACGATTAATTTATTTTGGAGCACTTTTTCAGCAA 4864
||||| 2774 CATGACTAATTAAGAACAGAACATTAATTTA--TTTTCGAGCACTTTTTCAGCTA 2825
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RESULT 5

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US-09-801-368-375
; Sequence 375, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Mline, Todd
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 375
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-375
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Query Match 2.1%; Score 111.8; DB 10; Length 2154;
Best Local Similarity 55.2%; Pred. No. 1.2e-17;
Matches 240; Conservative 0; Mismatches 192; Indels 3; Gaps 1;
QY 3762 AGCATTTCTCTTGTATGAGCTCAAGATGTGGAAGTGGAACTTGAATGAGCTGTGTA 3821
||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111
DB 1386 AGCCAATTCTGTATGAGATTAATGACGAGAGAACAAACAGAAATTAATGAAGATGTTGG 1445
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QY 3822 ACAGTGAATTAATGTCAGAAACATCTTCTGAGCAAGAAAGTAGTAGAACACTAAG 3881
||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111
DB 1446 GGGGCTAATGATCAACAAAAACCAATCAAAATATTCACAGAAAGATGTGATGCTTACA 1505
||||| 3882 AGAAGAGATTAAGATATATAGCATCATGATCCAAACATCATTTAGATGTGGAGC 3941
||||| 1506 GCATGAATTAATTAATTAAGAGATTACATCATGAGAACATTTACTTAATTAATGTGC 1565
||||| 3942 CAGGTGTGAAGAGCAATTAATCACTCTCATTTGAATGATGAGCGGGGATCGGTGCG 4001
||||| 1566 TTCTCAAGAGCGGGAATTAATTTTCTTGAATACGTTCCGCGGGTTCGGTTTC 1625
||||| 4002 TCATTGCTGAGTAATTAATGAGACCTTCAAGAAATCATTTACAGAGATGTCAAG 4061
||||| 1626 CTCATGCTGAATTAATTAAGTTCATTTGAGGATCAGTATTAATTTCACTAGGCA 1685
||||| 4062 GTTACCGCGCGCTTCTGATCTCATGAAAAACCAATCATTTACAGAGATGTCAAG 4121
||||| 1686 AATAGTGAATGGGTGCTGCTAATTTGCATTAAGAAACATTAATTCACAGAAATCAAGG 1745
||||| 4122 TGCATTTGCTAATTAATGACAGCACTGTGACAGACTAAGAAATTCAGATTTGAGACTGC 4181
||||| 1746 TCGAATTAATTTGATGATATCAAGCT---TCCGTAATAATTAATTAATTTGCTATTTC 1802
||||| 4182 AGCCAGTTGGCATC 4196
||||| 1803 AAAAAAATTAATCAAC 1817
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RESULT 6

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US-09-801-368-51
; Sequence 51, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Mline, Todd
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
; LENGTH: 4437
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-51
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Query Match 1.5%; Score 81; DB 10; Length 4437;
Best Local Similarity 50.8%; Pred. No. 9.4e-10;
Matches 223; Conservative 0; Mismatches 210; Indels 6; Gaps 1;
QY 3733 TGCGTGAAGGTCAACAGATAGCGCTTGGAGCATTTCTTCTGTTATCAGGCTCAAGAT 3792
||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111 ||| 1111
DB 3522 TCGATGAAGGATGAATGATTAAGGAAGGATCTTCGCGCTGTTATTTATGTTAAAC 3582
||||| 3733 GTGGAACTGGAACCTTTAATGCGCTGTAAACAGGTGACTTATGTCAGAAACATCTTCT 3852
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DB 3583 GTTACTACAGGTAGATGATGCGCTTACAGAGTTAGGTCCTCCCAAGTATAGCTCACAA 3642
QY 3853 GACCAAGAAAGAGTA-----GTAGAAGCAGCTAGAGAGAGATAGATAGATAGAGCCAT 3906
DB 3643 AATGAAGCCATTCTAGTACCGTGAAGCATTTAAGATCTAAGATGCTCAGGTTAAAGAT 3702
QY 3907 CTGATATCTCAACATCATTTAGGATTTGGAGCCAGCTGTGGAAGAGCAATTAACAT 3966
DB 3703 TTGATCATCTTATATATTTGTCATACTTACTAGTTTGTAGATATAAACAATATTTACAGT 3762
QY 3967 CTGTCTATGTAATGAGATGGAGGGGATCGGTGCTCATTTGCTGATTAATATAGAGCC 4026
DB 3763 TTGTTTAAATAATATGTGTGTGGCTCGTGGATCCTTGATTAAGATGATAGAGA 3822
QY 4027 TTCAAGAAATCAGTATGTTATTAATACATGACAGTACTGCTCCGTGGCTTTGCTATCTC 4086
DB 3823 TTGATGAAGACGTTGATCAACAATTTAACAACAGATATTTAAAGATTTGGCTATACCTA 3882
QY 4087 CATGAAGAACCAATCATTCACAGAGATGTCAAGAGTGCCTAATTTGCTAATTTGACGACT 4146
DB 3883 CACTCGAAAGGTATTTCCACAGAGATATGAGCAGCAACCTTATTTGATCAAGAT 3942
QY 4147 GGTCAAGACTAAGAAATG 4165
DB 3943 GGTATCTGCATAATTCAGTG 3961

RESULT 7

US-10-000-864-11
Sequence 11, Application US/10000864
Patent No. US20020146798A1
GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
FILE REFERENCE: CPT-085CPC
CURRENT APPLICATION NUMBER: US/10/000,864
CURRENT FILING DATE: 2001-10-31
EARLIER APPLICATION NUMBER: 09/423,890
EARLIER FILING DATE: 2000-06-03
EARLIER APPLICATION NUMBER: PCT/US99/05556
EARLIER FILING DATE: 1999-03-15
EARLIER APPLICATION NUMBER: USN 60/078,153
EARLIER FILING DATE: 1998-03-16
EARLIER APPLICATION NUMBER: USN 60/099,165
EARLIER FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 3332
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (332)..(2209)
US-10-000-864-11

Query Match 1.4%; Score 73.6; DB 12; Length 3332;
Best Local Similarity 49.8%; Pred. No. 5.5e-08;
Matches 327; Conservative 0; Mismatches 314; Indels 15; Gaps 5;

QY 3704 CAAACACACCGTATAGAGAGACATGATGGCTGAAGGTCAACAGATAGGCGCTTGAG 3763
DB 1386 CAACCAATCTCTAGTGTCCCATCAATTTGGCTGGGGAAGCTCTCGTGAAGGTG 1445
QY 3764 CATTTCCTTTCTGTATCAGGCTCAAGATGTGGAACTTGAATCTTAACTTTAAAC 3823
DB 1446 CCGTCGGCAGGCTCTACTTGTCTATATGTGACACAGACGTAAGCTTCTTAAGC 1505
QY 3824 AGGTGACTTATGTGAGAAACACATCTCTGAGCAAGAAGAGTAGTAGAAGCACTAAGAG 3883
DB 1506 AGGTCCAGTTTGACCCAGATA---GTCTTAGACAGCAAGAGAGTAGAGTCTTGAGAT 1562

QY 3884 AAGGATAGAGATGATGACCATCTGAATTCACAAATCATTTAGATGTTGGAGCCA 3943
DB 1563 GTGATATCCAGTTCTGAAGAACCTGCAGCATGAGCCATTTGCTAGTACTAGCGTGCC 1622
QY 3944 CG-----TGTGAGAAAGCAATTAACATCTCTTCATTTGAATGATGCGAGGGGATCGG 3997
DB 1623 TGGCGGACCGGTCTGAAGAAATCTCTACCAATCTTATGGAATATATCCAGGGGGCTGTG 1682
QY 3998 TGGCTCATTTGCTGAGTAATATGAGAGCCCTTCAAGAGATGAGTATATTAATACACTG 4057
DB 1683 TAAAGACCACTTAAGAGCTTACGAGCTCTGACAGAGATGTACCCGCAATGACACC 1742
QY 4058 AACAGTACTCCGTGGCTTTCGTATCTCATGAAACCAATCATTTACAGAGATGTCA 4117
DB 1743 GCGAGATTTGAGAGGCGATGTACATCTGCACACACATATGTTGATGGGACATCA 1802
QY 4118 AAGTGGCAATTTCTTAATGACAGCACTGCTCAGAGACTAAGATTTGAGATTTGGAG 4177
DB 1803 AGGAGGCCAATATCTCCGAGACTCAGCTG--GAATGTGAACCTTGGGATTTGGGG 1859
QY 4178 CTGAGCCAGGTTGGCATCAAAAGAACTGTGACAGAGAGTTTCAAGGACATTAAGTG 4237
DB 1860 C--CAGCAACGCTTAAGACCATCTGATGTCAAGGACAGGCAATTTGCTGTCTGCTG 1916
QY 4238 GGACAAATGCAATTTATGACACCTGAGGTACTAAGAGTCAACAGTATGAGAGAGCTGTG 4297
DB 1917 GCACACCTACTAGATGATGCTGAGTCAATCAGTGGCGAGGCTATGAGAAAGGACAG 1976
QY 4298 ATGTATGAGAGTGTGGCTGTGCTATTTATGAATAGGCTTGTGCAAAACCACTATG 4353
DB 1977 ACGTGTGAGGCTGTGGCTGTACTGTGTGAAATGCTGACAGAGAAACCACTTTGG 2032

RESULT 8

US-10-000-864-9
Sequence 9, Application US/10000864
Patent No. US20020146798A1
GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
FILE REFERENCE: CPT-085CPC
CURRENT APPLICATION NUMBER: US/10/000,864
CURRENT FILING DATE: 2001-10-31
EARLIER APPLICATION NUMBER: 09/423,890
EARLIER FILING DATE: 2000-06-03
EARLIER APPLICATION NUMBER: PCT/US99/05556
EARLIER FILING DATE: 1999-03-15
EARLIER APPLICATION NUMBER: USN 60/078,153
EARLIER FILING DATE: 1998-03-16
EARLIER APPLICATION NUMBER: USN 60/099,165
EARLIER FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 2465
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (427)..(2283)
US-10-000-864-9

Query Match 1.4%; Score 71; DB 12; Length 2465;
Best Local Similarity 47.8%; Pred. No. 2e-07;
Matches 333; Conservative 0; Mismatches 355; Indels 9; Gaps 4;

QY 3666 ACAGATACACACAGACTCTACAGGACATATACAAAGCAAAACCGTATAGAGAGA 3725
DB 1425 AGAACATCTCACTTTGACTGTGACAGACATCAGCCACCGGCTTCACTGACAGCTCC 1484
QY 3726 CACTGAATGGCTGAAGGTCACACAGATAGGCTTGAGACATTTTCTTCTTATACAGG 3785

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Db 1485 GACCAACTGGACACTGGGACGCTGCTTGGCCAGGAGCTTTGGTAGGCTTACTCTG 1544
Qy 3786 TCAAGATGTTGGGACACTGTAACCTTTATGCGCTTTAAACAGTGACTATCTAGAAACAC 3845
Db 1545 CTATGATGTTGATACCGGAAAGAGCTGCTTTAAGCAAGTTCACTTAACCCCTAGAG 1604
Qy 3846 ATCTTCTGAGCAAGAAAGATGATAGACACTAGAGCAAGATTAAGATGATGAGCA 3905
Db 1605 CCCAGAGACCAAGGAGATTAATGCACTTGAAGTGTAAATTCAGTTGTAAAACTT 1664
Qy 3906 TCTGATCATCCCA--ACATCATTAGATGTGGAGCCACGCTGTGAGAGAGCAATTACA 3964
Db 1665 GTTGATGAGCCAAATTTGTCAGTATTTATGCTGTTGAGGAGATCCCTCAGAGAAAACT 1724
Qy 3965 ATC--TCTTCAATGAATGGATGGAGGGGATCGTGCTCATTTGCTGATTAATATG 4022
Db 1725 TTCCATCTTTATGAGCTCTCGCAGGGGGTTCAATTAAGACACMAAAGCCTAAG 1784
Qy 4023 ACCCTTCAAAAGATCAGTATTTATTAACACTGACAGCAATTAATCTCGCTTTCGA 4082
Db 1785 ACCTCTTACTGAAACGTGACGAGGAATACACCGCTCAGATTTCTGAGGGGCTCCATTA 1844
Qy 4083 TCTCCATGAAAAACAATCATTCACAGAGATGCAAAAGGTGCCAATTTGCTAATTGACAG 4142
Db 1845 TTTCATTAATTAATGATTTGCTCATAGAGATATCAAGAGACAAATATCTTAAGGATTC 1904
Qy 4143 CACTGCTCAGAGACTAAGATTTGCAAGATTTTGGAGCTGACGCGAGTTGGCATCAAAAG 4202
Db 1905 CACAGGCAATATC--AAGTAGAGACCTTTGGGGCTAGTAAGAGGCTTCAAGACATCT 1962
Qy 4203 AACTGCTGAGAGAGCTTTCAGGACAAATTAACCTGGGACAAATGCAATTAATGCACTGA 4262
Db 1963 CTCTGACGACAGGAT---GAAGTCTCTCAGAGCGACGCCAATCTGATGATGCTTA 2018
Qy 4263 GGTACTAAGAGGCAACACTATGAGAGAGAGCTGTGATGTAGAGTGGCTGCTAAT 4322
Db 2019 GGTTCATCAGTGAGAGGCTATGAGAGAAAGACAGACATCTGAGTGTAGCATGTA 2078
Qy 4323 TATAGAAATGCTGTGCAAAACCAACCATGGAATGCA 4359
Db 2079 GGTAAGAAATGTAACCTGAAAAGCACACCTTGGGCTGAA 2115
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RESULT 9
US-10-000-864-3
; Sequence 3, Application US/10000864
; Patent No. US20020146798A1
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
; FILE REFERENCE: CPT-085CPC
; CURRENT APPLICATION NUMBER: US/10/000,864
; EARLIER FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: USSN 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: USSN 60/099,165
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(1980)
US-10-000-864-3
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Query Match 1.3%; Score 70.4; DB 12; Length 2013;
Best Local Similarity 47.9%; Pred. No. 2.4e-07;
Matches 327; Conservative 0; Mismatches 346; Indels 9; Gaps 4;
Qy 3681 GACCTACAGGACATACCAAAAGCAAAACCGTATACAGAAAGACATGAGTGTGAA 3740
Db 1137 GACTGTACACAGACATACGACCACCATGCGCTTACCTGAGCTCGGACCACTGAGACT 1196
Qy 3741 AGTCAACAGATAGAGCTTGGAGCAATTTCTTTATATCAGAGCTCAAGATGTGGGAAC 3800
Db 1197 GGGCAAGCTGCTGGCAAGAGAGATTTTGTAGGGCTACCTGTGTATGATGTGATAC 1256
Qy 3801 TGGACTTAAATGCTGTTAAACAGTACTTATGTGCAAAACACATCTTGTGACAGAGA 3860
Db 1257 CGGAAGAGCTGCGCTGTTAAGCAAGTTCAGTTAAACCTTGAGAGCCAGAGACAGCA 1316
Qy 3861 AGAGTAGTAGAAGCACTAAGAAAGAGATTAAGATAGACCAATCTAATCAATCCAA- 3919
Db 1317 GGAAGTAAATGCACTTGAGTGTGAATTCAGTTGTGAAAACTTGTTCATGAGCGAAT 1376
Qy 3920 ACATCATTAAGATGTGGAGCCACGCTGAGAAAGCAATTAACAATC--TCTCATTTGA 3977
Db 1377 TGTTCAGTATTATGCTGTTTGAAGGATCTCAGAGAAACACTTTCATCTTATGGA 1436
Qy 3978 ATGATGSCAGGGGATCGTGCTCATTTGCTGATTAATATGAGCCCTCAAGAAATC 4037
Db 1437 GTATATGCCAGGGGCTTCAATTAAGGACCACTAAGAGCCAGGAGCTTACTGAGAA 1496
Qy 4038 AGTAGTATTAACTACACTGAACAGTATCCGCTGGCTTGTGATATCTCATGAAACCA 4097
Db 1497 CGTAGCAGGAAGTACACCGCTCAGATTTCTGAGAGGGGCTCAATTTATGCAATGTAAT 1556
Qy 4098 AATCATTTACAGAGATGTCAAAAGTGCCAAATTTGCTAATTTGACAGACCTGTGAGACT 4157
Db 1557 GATTCGCTATAGAGATATCAAAAGGACAAATTTCTTAAGAGATTCACAGGCAATATC-- 1614
Qy 4158 AAGATTTGCAATTTTGGAGCTGACAGCCAGGTGGCATCAAAAGAACTGTGCAAGAGA 4217
Db 1615 AAGTTAGAGACTTTGGGGCTGATTAACCGCTTACAGACCATCTGCTCTCAGGACAGGA 1674
Qy 4218 GTTTCAGGACAAATTAACCTGGGACAAATTCATTTATGGAAGCTGAGAGTCAAGAGTCA 4277
Db 1675 AT---GAAGTGTACAGGACCGCATACGATGAGTGTGCTGCTATTAATGAATGGCTTG 1730
Qy 4278 ACAGTATGGAAGAGCTGTGATGTAATGAGTGTGCTGCTGCTAATTAATGAATGGCTTG 4337
Db 1731 AGGCTATGGAAGAAAGACAGACATCTGAGTGTAGCATGTAGAGTGTGAATGCTTAAC 1790
Qy 4338 TGCAAAACCAACATGGAATGCA 4359
Db 1791 TGAAAAGCCACCTTGGGCTGAA 1812
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RESULT 10
US-09-967-624-1
; Sequence 1, Application US/09967624
; Patent No. US20020142325A1
; GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Wu, Jun
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: PAK2: Modulators of Lymphocyte Activation
; FILE REFERENCE: 021044-000700US
; CURRENT APPLICATION NUMBER: US/09/967,624
; EARLIER FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/280,647
; NUMBER OF SEQ ID NOS: 19
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;; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, polypeptides, &
;; FILE OF INVENTION: Antibodies
;; FILE REFERENCE: PTO20P1
;; CURRENT APPLICATION NUMBER: US/09/836,392
;; CURRENT FILING DATE: 2001-04-18
;; PRIOR APPLICATION NUMBER: PCT/US00/28066
;; PRIOR FILING DATE: 2000-10-11
;; PRIOR APPLICATION NUMBER: 60/159,542
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/165,914
;; PRIOR FILING DATE: 1999-11-17
;; PRIOR APPLICATION NUMBER: 60/189,027
;; PRIOR FILING DATE: 2000-03-14
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 2380
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-836-392-5

Query Match 1.3%; Score 65.6; DB 9; Length 2380;
Best Local Similarity 51.5%; Pred. No. 4.3e-06;
Matches 202; Conservative 0; Mismatches 184; Indels 6; Gaps 2;

QY 3968 TCTTCATTGATGATGCGAGGGGATCGGCTCATTTGCTGAGTAATATGAGCCT 4027
DB 175 TATTTATGGAATATATGCGAGGGGCTTCATTTAAGGACCAATTAAGCATATGCGCTC 234
QY 4028 TCAAGAAATCACTACTTATTAATCACTGACAGAGTTACTCGGCTTGGTATCTTC 4087
DB 235 TTACTGAGAACTGACTGAGAAATACCCGTCAGATTTGAGAGGTGTCATTTATTTGC 294
QY 4088 ATGAATACCAATTCATTCACAGAGATGTCNAAGTGCCATTTGCTAATTTGACAGACTG 4147
DB 295 ACAGTAATATGATTTGTCATAGATATCAAGAGGCAATATTCGCGAGATTCACAG 354
QY 4148 GTCAAGAGCTAAGATTTGCAATTTTGGAGCTGCAGCCAGGTTGGCATCAAAAGCACTG 4207
DB 355 G---CAAGCTCAACATGAGAGATTTGGGGCCAGCAAGGCTTCAGACCATCTGCTCT 411
QY 4208 GTGCAAGAGATTTTCAGGAGCAATTAATCTGAGCAATTCATTTTGGCACTGCTTAT 4267
DB 412 CAGGACACAGAGATGAAGTCTG---TCACGGGACACACCATCTGATGAGCCCTGAAGTCA 468
QY 4268 TAAGAGGTCAACAGTATGAGAGAGCTGTGATGATGAGAGTGTGGCTGTCTATTATAG 4327
DB 469 TCAGTGCAGAAAGCTATGAGAGAAAGACAGACATCTGAGTGTGATGTACTGTGTAG 528
QY 4328 AATGGCTTTGCAAAACCAACCATGGAATGCA 4359
DB 529 AATGCTAATGTAAGAGCGCTTGGCTGAA 560

RESULT 13
US-10-000-864-5
;; Sequence 5, Application US/10000864
;; Patent No. US20020146798A1
;; GENERAL INFORMATION:
;; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
;; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
;; TITLE OF INVENTION: AND USES THEREFOR
;; FILE REFERENCE: CPT-083CPC
;; CURRENT APPLICATION NUMBER: US/10/000,864
;; CURRENT FILING DATE: 2001-10-31
;; EARLIER APPLICATION NUMBER: 09/423,890
;; EARLIER FILING DATE: 2000-06-03
;; EARLIER APPLICATION NUMBER: PCT/US99/05556
;; EARLIER FILING DATE: 1999-03-15
;; EARLIER APPLICATION NUMBER: USSN 60/078,153
;; EARLIER FILING DATE: 1998-03-16
;; EARLIER APPLICATION NUMBER: USSN 60/099,165
;; EARLIER FILING DATE: 1998-09-04

;; NUMBER OF SEQ ID NOS: 38
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 1935
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (25)..(1902)
US-10-000-864-5

Query Match 1.2%; Score 64.6; DB 12; Length 1935;
Best Local Similarity 52.6%; Pred. No. 6.7e-06;
Matches 211; Conservative 0; Mismatches 184; Indels 6; Gaps 3;

QY 3953 AGAGCAATTCATATCTCTCATTTGATGATGAGGAGGAGTGGCTCATTTGCTGA 4012
DB 1331 AGAAGATCTCTACCATCTTTATGAGATATGTCAGGGGCTCTGTAAGACCACTTGA 1390
QY 4013 GTAATATGAGACCTTCAAGAAATGAGTATTAATTAATCACTGACAGTATCTCCGTG 4072
DB 1391 AGGCTTACGAGCTCTGACAGAGAGTGTGACCCGCAAGTACACCGGAGATTCTGAGG 1450
QY 4073 GCTTTTCTATCTCATGAAACCAATTCATTCACAGAGATGTCAAAGTCCCAATTTGC 4132
DB 1451 GCATGTCATATCTGACAGACCAATGATTTGTCATCGGACATCAAGGAGCAATATCC 1510
QY 4133 TAATGACAGACCTGTCAGACTAAGAAATTCAGAAATTTGGACTGACGAGGTTGG 4192
DB 1511 TCCGAGACTCAGCTGG---GAATGTGAAGCTTGGGATTTTGGGGC--CAGCAACACT 1565
QY 4193 CATCAAAAGAACTGGTGCAGAGAGATTTTCAGGACAAATTAATGAGCAATTCATTTA 4252
DB 1566 ACAGACCATCTCATGATGAGGAGGAGGATTCGCTCTGTCATGAC -ACACCTACTGGA 1624
QY 4253 TGGACCTGAGTACTAAGAGGTCAACAGTATGAAAGAGCTGTGATGATGAGAGTGTG 4312
DB 1625 TGAATCTGTAATCATCATGCTGCGAGGCTATGAGAAAGGACGAGTGTGAGACTGG 1684
QY 4313 GCTGTCTATTATGAATATGCTTGTGCMAAACCAACCATGG 4353
DB 1685 GCTGTACTGTGTGATATGCTGACAGAGAAACCACTTGG 1725

RESULT 14
US-09-976-740-48
;; Sequence 48, Application US/09976740
;; Publication No. US20020194633A1
;; GENERAL INFORMATION:
;; APPLICANT: Lees, Ann M.
;; APPLICANT: Lees, Robert S.
;; APPLICANT: Law, Simon W.
;; APPLICANT: Ajlona, Anibal A.
;; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;; TITLE OF INVENTION: ATHEROSCLEROSIS
;; FILE REFERENCE: 10797-004001
;; CURRENT APPLICATION NUMBER: US/09/976,740
;; CURRENT FILING DATE: 2001-10-12
;; PRIOR APPLICATION NUMBER: 09/616,289
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 08/979,608
;; PRIOR FILING DATE: 1997-11-26
;; PRIOR APPLICATION NUMBER: US 60/031,930
;; PRIOR FILING DATE: 1996-11-27
;; PRIOR APPLICATION NUMBER: US 60/048,547
;; PRIOR FILING DATE: 1997-06-03
;; NUMBER OF SEQ ID NOS: 53
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 48
;; LENGTH: 2561
;; TYPE: DNA
;; ORGANISM: Oryctolagus cuniculus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-09-976-740-48

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Query Match
Best Local Similarity 49.7%; Pred. No. 3.2e-05; Length 2561;
Matches 215; Conservative 0; Mismatches 213; Indels 5; Gaps 2;

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QY 49 CCGGGCCAGAGGCTACAGCCCTGAGGCGAGGCGGCGAGAGGCTCAAGGCGAGC 108
Db 589 CCCCCCGGGGGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 648
QY 109 AGCGCGCCCGCGGCTGCGCGGAGCTGCTGCGGAGCGGCGGCGCGCGCGCG 168
Db 649 CGCCCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 708
QY 169 GCGGACGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 228
Db 709 CCGCTGCGCGCGCACAGCGCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 764
QY 229 GAGCAGCGCGCTCTTCTTGGCGGCTCAAGCGCGGCTCTTCAAGTCCCGCGCGAG 288
Db 765 CAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 824
QY 289 CCGCGGAGCGAGCGGCGGAGTGGGAGCGGCTTCCAGCGCTGTGGCGGCGCGCG 348
Db 825 CCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 883
QY 349 GAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408
Db 884 GCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 943
QY 409 GCCTCGAGTCCCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 468
Db 944 GCGACGCGCGCGCGCGAGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1003
QY 469 CCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
Db 1004 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1016

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RESULT 15
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020129388a1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-10-023-529-48

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Query Match
Best Local Similarity 49.7%; Pred. No. 3.2e-05; Length 2561;
Matches 215; Conservative 0; Mismatches 213; Indels 5; Gaps 2;

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QY 49 CCGGGCCAGAGGCTACAGCCCTGAGGCGAGGCGGCGAGAGGCTCAAGGCGAGC 108
Db 589 CCCCCCGGGGGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 648
QY 109 AGCGCGCCCGCGGCTGCGCGGAGCTGCTGCGGAGCGGCGGCGCGCGCGCG 168
Db 649 CGCCCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 708
QY 169 GCGGACGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 228
Db 709 CCGCTGCGCGCGCACAGCGCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 764
QY 229 GAGCAGCGCGCTCTTCTTGGCGGCTCAAGCGCGGCTCTTCAAGTCCCGCGCGAG 288
Db 765 CAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 824
QY 289 CCGCGGAGCGAGCGGCGGAGTGGGAGCGGCTTCCAGCGCTGTGGCGGCGCGCG 348
Db 825 CCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 883
QY 349 GAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408
Db 884 GCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 943
QY 409 GCCTCGAGTCCCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 468
Db 944 GCGACGCGCGCGCGCGAGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1003
QY 469 CCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
Db 1004 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1016

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Search completed: December 28, 2002, 01:13:49
Job time : 335 secs

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    /cell_line="NT2"
    /note="Vector: pME18SF3; mRNA from NT2 neuronal precursor
    cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT    263 a    169 c    180 g    220 t      4 others
ORIGIN
Query Match      15.0%; Score 787.8; DB 9; Length 836;
Best Local Similarity 98.3%; Pred. No. 3e-158;
Matches 825; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

OY 4011 GAGTAAATATGAGCCTTAAAGAACATAGTATTAATCACTACAGACAGTACTCCG 4070
    1 GAGTAAATATGAGCCTTAAAGAACATAGTATTAATCACTACAGACAGTACTCCG 60
OY 4071 TGGCCTTGTATCTCCATGAACCAATCATTCACAGAGATGTCAGAGTCCCAATT 4130
    61 TGGCCTTGTATCTCCATGAACCAATCATTCACAGAGATGTCAGAGTCCCAATT 120
OY 4131 GCTAAATGACAGCAGTGTGACAGACTAAAGAAATGTCAGATTTTGAGCTGCAGCCAGTT 4190
    121 GCTAAATGACAGCAGTGTGACAGACTAAAGAAATGTCAGATTTTGAGCTGCAGCCAGTT 180
OY 4191 GGCATCAAAAAGAACGTCGTGACAGAGAGTTTCAGGAGCAATTAATCTGGGCAATTGCATT 4250
    181 GGCATCAAAAAGAACGTCGTGACAGAGAGTTTCAGGAGCAATTAATCTGGGCAATTGCATT 240
OY 4251 TATGACACCTGAGGACTAAGAGGTCAACAGATGGAAGAGAGTGTATGAGAGT 4310
    241 TATGACACCTGAGGACTAAGAGGTCAACAGATGGAAGAGAGTGTATGAGAGT 300
OY 4311 TGGCTGTGTATATAGAAATGGCTTGTGCAAAACACCATGGAATGCGAAAAACATC 4370
    301 TGGCTGTGTATATAGAAATGGCTTGTGCAAAACACCATGGAATGCGAAAAACATC 360
OY 4371 CAATCATCTGCTTGTATATTAAGATTGCTAGTGCACACTAGCTCCATCCCTTC 4430
    361 CAATCATCTGCTTGTATATTAAGATTGCTAGTGCACACTAGCTCCATCCCTTC 420
OY 4431 ACATTTGTCTCTGTTTACGAGATGTGGCTCTGTTGTTTGAACCTTCAACCTCAGA 4490
    421 ACATTTGTCTCTGTTTACGAGATGTGGCTCTGTTGTTTGAACCTTCAACCTCAGA 480
OY 4491 CAGACCTCCATGAAGAGACTACTGAGCATCCAGTCTTTCGTAATGTTAGCCAAAT 4550
    481 CAGACCTCCATGAAGAGACTACTGAGCATCCAGTCTTTCGTAATGTTAGCCAAAT 540
OY 4551 TATGACATCACTACAGTAAAGAGATGCTCAACAGAGAAAAAACTGTGGGGA 4610
    541 TATGACATCACTACAGTAAAGAGATGCTCAACAGAGAAAAAACTGTGGGGA 600
OY 4611 ACCACATGATATTTACTAGCCATGATGCCACTGAACAGCTATGAAAGAGCCACTGGG 4670
    601 ACCACATGATATTTACTAGCCATGATGCCACTGAACAGCTATGAAAGAGCCACTGGG 660
OY 4671 GAACCTTACCTAAGTATGTGATGCAAAATCATGATGCTGCTAAGCTCAGTATGCAA 4730
    661 GAACCTTACCTAAGTATGTGATGCAAAATCATGATGCTGCTAAGCTCAGTATGCAA 719
OY 4731 AAGCCCAAACTAGTCAGAAACTGTAAACTGCTTTCAAAAGACTGGCCCTAGGTGAA 4790
    720 AAGCCCAAACTAGTCAGAAACTGTAAACTGCTTTCAAAAGACTGGCCCTAGGTGAA 778
OY 4791 CAGAAAACAATGAAGTTGATGACTAAATTTGACAGAAAGCATATTTTATTTTGA 4849
    779 CAGG-AAACCATGAATTTNCATGACTAAATTTGACAGAAAGCATATTTTATTTTGA 836

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RESULT 2
LOCUS      BM928438
DEFINITION AGENCOURT_6699830 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770238
ACCESSION  BM928438
VERSION     BM928438.1 GI:19378817
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 1043)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM12832 row: p column: 15
            High quality sequence stop: 625.

FEATURES
  source
    1. 1043
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    /clone_id="IMAGE:5770238"
    /clone_1lb="NIH_MGC_121"
    /lab_host="DH10B"
    /note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI;
    Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
    fetal brains, female age 20 weeks, female age 24 weeks,
    and male age 26 weeks. Library is oligo-dT primed and
    directionally cloned (EcoRV site is destroyed upon
    cloning). Average insert size 1.7 kb. Insert size range
    0.7-3.5 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 017. Note:
    this is a NIH-MGC library."

BASE COUNT    318 a    187 c    190 g    348 t
ORIGIN
Query Match      13.0%; Score 682.4; DB 14; Length 1043;
Best Local Similarity 99.0%; Pred. No. 1.2e-135;
Matches 697; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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    1 GGTAGCAATTTATGCAATCACTACAGTAGAAACAGATGGTCTCAACAGAGAAAAA 60
OY 4601 CTT-GTGGGGAACACATTTATTTCTAGTGGCATGATGCCACTGAAACGTATGAAAG 4659
    61 CTTGGTGGGGAACACATTTATTTCTAGTGGCATGATGCCACTGAAACGTATGAAAG 120
OY 4660 AGGCCAGTGGGGAACCTTACTAAGTATGTGATTTGACAAATCATGATCTGTAAC 4719
    121 AGGCCAGTGGGGAACCTTACTAAGTATGTGATTTGACAAATCATGATCTGTAAC 180
OY 4720 TCAGTATGCAAAAGCCCAACTAGTGCAGAAACTGTAACTGCTTCAAGAACTGG 4779
    181 TCAGTATGCAAAAGCCCAACTAGTGCAGAAACTGTAACTGCTTCAAGAACTGG 240
OY 4780 CCTAGGTAAACAGAAACAATGAAGTTTGCATGATTAATTTGAGAAAGCATATTTTA 4839
    241 CCTAGGTAAACAGAAACAATGAAGTTTGCATGATTAATTTGAGAAAGCATATTTTA 300
OY 4840 TTTTGTGAGCAGCTTTTCAGCAATATTTAGCGGCTGAGGGGCTCAGATCTATTAAT 4899

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Db 301 TTTTGTGGAGCTTTTTCAGCAATATAGCGGCTGAGGGGCTCAGGATTTATTTTAT 360
Qy 4900 ATTCAATTAATTTTCATTTTCATATAGTGATCAACAAGCAGGGGCTTCGAATTCGTT 4959
Db 361 ATTCAATTAATTTTCATTTTCATATAGTGATCAACAAGCAGGGGCTTCGAATTCGTT 420
Qy 4960 CAAATTTTGTGCTGCTGCTAATAATCAGTATCTGCTCTTTTAAAGTCAGATGCTA 5019
Db 421 CAAATTTTGTGCTGCTGCTAATAATCAGTATCTGCTCTTTTAAAGTCAGATGCTA 480
Qy 5020 TGAGTACAAATACATATATTTTAAAGTGAATACCTTATGAGCCACAGTGA 5079
Db 481 TGAGTACAAATACATATATTTTAAAGTGAATACCTTATGAGCCACAGTGA 540
Qy 5080 CTTTATTTTCTTAATAATACAGGCGAGTGTGCTCATTTGCTATTTTACTGTTGGCCA 5139
Db 541 CTTTATTTTCTTAATAATACAGGCGAGTGTGCTCATTTGCTATTTTACTGTTGGCCA 600
Qy 5140 TTTCAATTCGTTTGGAAATATATGTTTGTATTTTCATGTTTATTTACATTCATTTTG 5199
Db 601 TTTCAATTCGTTTGGAAATATATGTTTGTATTTTCATGTTTATTTACATTCATTTTG 660
Qy 5200 TTTTTCAGGGAAGCTGATCTTTTTCACAAACCAAAAAA 5243
Db 661 TTTTTCAGGGAAGCTGATCTTTTTCACAAACCAAAAAA 704

RESULT 3
LOCUS AL042445 653 bp mRNA linear EST 29-FEB-2000
DEFINITION DKFZP434D2221.F1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION AL042445
VERSION DKFZP434D2221.5, mRNA sequence.
KEYWORDS AL042445.1 GI:5421814
SOURCE EST.
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 653)
COMMENT Blum H., Bauersachs S., Mewes H.W., Gassenhuber J. and Wiemann S.
Unpublished (1999)
Contact: Blum H
MIPS
Am Kioferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFZP434D2221) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: Clone@rzpd.de.
location/Qualifiers
1. 653
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP434D2221"
/clone_id="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab host="DH10B"
/notes="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 199 a 121 c 157 g 173 t 3 others
ORIGIN
Query Match 11.4%; Score 598; DB 9; Length 653;
Best Local Similarity 98.6%; Pred. No. 1,5e-117;
Matches 624; Conservative 0; Mismatches 6; Indels 3; Gaps 2;
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Qy 3856 CAGAGCAAGTAGTAGAAGCACTAAGAGAGATAGATAGATGAGCCATCTGATCAT 3915
Db 1 CAGAGCAAGTAGTAGAAGCACTAAGAGAGATAGATAGATGAGCCATCTGATCAT 60
Qy 3916 CCAAAACATATAGGATGTTGGGAGCCACGCTGTGAGAGACAAATTAACCTCTTCAT 3975
Db 61 CCAAAACATATAGGATGTTGGGAGCCACGCTGTGAGAGACAAATTAACCTCTTCAT 120
Qy 3976 GAATGATGAGGAGGAGGATGCTGCTCATTTGCTGAGATTAATAGAGCCCTCAAGAA 4035
Db 121 GAATGATGAGGAGGAGGATGCTGCTCATTTGCTGAGATTAATAGAGCCCTCAAGAA 180
Qy 4036 TCAAGTATTAATACATACAGTGAACAGTACTCGTGGCTTTGCTATCTCAGTAAAC 4095
Db 181 TCAAGTATTAATACATACAGTGAACAGTACTCGTGGCTTTGCTATCTCAGTAAAC 240
Qy 4096 CAAATCATTCACAGAGATGTAAGAGTCCCAATTTGCTATTTGACAGACATGCTCAGAA 4155
Db 241 CAAATCATTCACAGAGATGTAAGAGTCCCAATTTGCTATTTGACAGACATGCTCAGAA 300
Qy 4156 CTAAGAAATTCAGATTTTGGAGCTCAGCCAGGTGGCATCAAAAGAACTGGTCAGGA 4215
Db 301 CTAAGAAATTCAGATTTTGGAGCTCAGCCAGGTGGCATCAAAAGAACTGGTCAGGA 360
Qy 4216 GAGTTTCAGGACAAATTCAGTGGGACAAATTCATTTATGGAACCTGAGTACTAAGAGT 4275
Db 361 GAGTTTCAGGACAAATTCAGTGGGACAAATTCATTTATGGAACCTGAGTACTAAGAGT 420
Qy 4276 CAACAGTATGGAAGAGAGCTGTGATGTATGAGAGTGTGCTGTGCTATTTATGAAATGCT 4335
Db 421 CAACAGTATGGAAGAGAGCTGTGATGTATGAGAGTGTGCTGTGCTATTTATGAAATGCT 480
Qy 4336 TGTGCAAAACCAACCATGGAATGAGAAACACATCCATCATCTGCTTGTATTTAAG 4395
Db 481 TGTGCAAAACCAACCATGGAATGAGAAACACATCCATCATCTGCTTGTATTTAAG 540
Qy 4396 ATTGCTAGTGCACACTGCTGCTCATGATCCCTTCACATTTGCTGCTGTTTACA--G 4453
Db 541 ATTGCTAGTGCACACTGCTGCTCATGATCCCTTCACATTTGCTGCTGTTTACAAGA 600
Qy 4454 ATGCGCTCTCTGCTGTTT--AGAACTCAACCT 4485
Db 601 ATGCGCTCTCTGCTGTTT--AGAACTCAACCT 633

RESULT 4
LOCUS B1654958 868 bp mRNA linear EST 12-SEP-2001
DEFINITION 603283220.F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5327644 5'
ACCESSION B1654958
VERSION B1654958.1 GI:15569194
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: L1AM11831 row: 9 column: 05
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	/clone_lib="NCI_GAP_Man4"		
	/tissue_type="tumor, gross tissue"		
	/dev_stage="5 months"		
	/lab_host="DH10B"		
	/note="Organ: mammary; Vector: PCMV-SPORT6; Site:1: salivary; Site:2: NCI: Cloned unidirectionally. Primer: oligo dt. library constructed by Life Technologies. Investigators providing samples: Jothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."		
BASE COUNT	220 a 230 c 264 g 154 t		
ORIGIN			
Query Match	11.1%, Score 583; DB 13; Length 868;		
Best Local Similarity	85.0%; Pred. No. 2.5e-114;		
Matches 664; Conservative 0; Mismatches 115; Indels 2; Gaps 1;			
QY	483 CGCCGGTGTGATGATGAGGAATTAAGAAACTCTCAAAAGGTTGCACAGATGATGATCG	542	
DB	64 CGCGAATCGAGAGATGAGAAATTAAGAAACCTCTCAAGAGACTGCAAGATGAGAGATCG	123	
QY	543 TCCAGAGGACGAATGATCAGGAGAGAAATCGAAGCAACCTGTATGCCAGCTGGAGCA	602	
DB	124 CCCGGAGGAGAAATGATCCGGGAGAACTCAAGCCGACCTGTATGCCGCTGGAGCA	183	
QY	603 CGAATGTTGGAAAGGAAATATAGCGAGGCGTGTGTGTTAAACCAATCCAGTTAA	662	
DB	184 CGAGTGTGTTGGAGAGAGAAACAGAGAGAGCCCTGTGTGTGTAAGCAATCCATTTAA	243	
QY	663 AGGAATGATGATCTGAAATGATCACTATTGACAGCTATGCTCCAGAGAGGTCCAGGCAAG	722	
DB	244 AGGAATGATGATCTGAAATGATCACTATTGACAGCTATGCTCCAGAGAGGTCCAGGCAAG	303	
QY	723 TGCAGCTTCACACAGCTTCCAAAGGCGGACGAGAGTCTCTCTGCACTCCCATTCAGG	782	
DB	304 TTCCCTCTGACACAGCCGCCCAAGGCGGACGAGAGCCCATCTCTGCACTCTCCGTCAGG	363	
QY	783 TCGCAGTGAATTCGATTCGACGAGTAAGGAGAAAAGAGTTTCCCGACGTGCTTT	842	
DB	364 GCGCTCGGTGAAGCCGGAATCCCGAGAGTGAAGAGAAAGAGTTCGCCGCTCTTT	423	
QY	843 TCAGAGTGGCAGATCAACACCCGCCGAAAGAGCCCTTCACCAAGTGGCTTCAACCTA	902	
DB	424 CCAGAGTGGCAGAAATCAACACCCGCCGAAAGAGCCCATCAACGAGTTCCTCCCTTA	483	
QY	903 TAGCCCTAGGAAACCAACCGCGGTGAACAAATGATGAGGCGGACAGTACTTACT	962	
DB	484 CAGCCCAAGAGAGACGAGACCGCGCGGTGAACAAATGATGAGAGCAGGCTGTACTCT	543	
QY	963 GCAGCAGATAGGCGCTTAACCTTTTCTGATGAGAGACAGCCCGACAGCAATTAATACG	1022	
DB	544 GCAGCAGATAGGAGAACCACTCTTCTGATGAGAGACAGCTCCAGCAATTAATACG	603	
QY	1023 GGTGTTATTGGGCTCTCAAACTGCAAGCTGTGACAGCTGGAACATTTCTATTCATCTCT	1082	
DB	604 GGTGTTATTGGGCTCTCAAACTGCAAGCTGTGACAGCTGTGACATTTCTATTCATCTCT	663	
QY	1083 ATTGTGATGCTCCGGGTGTTCAACTGAAACCTTCACACCCATGTTATGAGAGAAAAC	1142	
DB	664 GTTGTGATGCTCCGGGTGTTCAACTGAAACCTTCACACCCATGTTATGAGAGAAAAC	723	
QY	1143 TTT - - AAGAGATTTTGAAGTTGAGAGTTGTCTCGAAATTAATCAAGAGCGTAGCA	1200	
DB	724 TTTTAGAAACATTTTCAGGTTGAGAGTTGTTCCTCGAAATTAATCAAGAGCGTAGCA	783	
QY	1201 AGATCAAAAGCTCATCTCGTACACCATTCAGAAAGTTTGTTCACGCAATGCAATTCCT	1260	

Db	784	AGAACTCAAGCTTCATCCCGGAACACATCCAGAAAGTTGTCTCCGCGCTGCAAAATGCT	843
OY	1261 C 1261		
Db	844 C 844		
RESULT 5			
LOCUS	AJ450706	716 bp	mrna
DEFINITION	AJ450706 riken1 Gallus gallus cDNA clone 26c20r1, mRNA sequence.	linear	EST 19-APR-2002
ACCESSION	AJ450706		
VERSION	AJ450706.1	GI:20217927	
KEYWORDS	EST.		
SOURCE	chicken.		
ORGANISM	Gallus gallus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;		
	Phasianinae; Gallus.		
	1 (bases 1 to 716)		
REFERENCE	Buerstedde, J. M.		
AUTHORS	Gallus gallus bursa lymphocyte EST		
TITLE	Unpublished (2002)		
JOURNAL	Contact: Buerstedde JM,		
COMMENT	Cellular Immunology Heinrich-Pette-Institute Martinistr. 52, 20251 Hamburg, Germany Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.		
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Source	1..716		
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	/db_xref="taxon:9031"		
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	/clone_lib="riken1"		
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	/dex_stage="2-3 weeks old"		
	/note="CB inbred strain"		
BASE COUNT	226 a 132 c 175 g 182 t	1 others	
ORIGIN			
Query Match	10.4%; Score 544; DB 9; Length 716;		
Best Local Similarity	85.8%; Pred. No. 5.7e-106;		
Matches 615; Conservative	0; Mismatches 101; Indels 1; Gaps 1;		
OY	3546	GATGGAAGCTGAAGAAGAAGCTTTAGCAATTGCCATGGCAATGTGACGCTGCACAGA	3605
Db	1	GATGGAAGCTGAAGAAGAAGCTTTAGCTATTGCTATGGCAATGTGCTGATCTCAAGA	60
OY	3606	TGCCCTCCCAAGTGTCTCTCAGCTCAGCTGGAANAATGAGAAAGATATCATCATTTATCA	3665
Db	61	TGCCCTGCCAAATTAATTTCCCACTACAGGTGCAAAATGGTGAAGATATCATTAATTTCA	120
OY	3666	ACAGAGTACACACAGAGACTCTACACAGACATACCAAAACCAACCGTATAGAGAAGA	3725
Db	121	GCAGATATACACAGAAACTCTGCTCGACATACCAAAAGCAATCATTCACAGGAAGA	180
OY	3726	CACGTGAATGGCTGAAGAAGTCAACAGATAGCCCTTGAGACATTTCTTGTATCAGCG	3785
Db	181	TGCAGAAATGGCTTAAGGTACAGCAAAATTTGCTTGAGACTTCTCTCTCTTACCAAGC	240
OY	3786	TCAAGATGTGGAACTGGAACATTTAATGGCTTAAACAGAGCACTTAATGTCAAGAAC	3845
Db	241	TCAAGATGTAGGAACAGGACATTTAATGGCTTAATAAAGGTGACATATGTACAGGAAC	300
OY	3846	ATCTCTAGCAAGAAGAAGTAGTAGAAGCACTAAGACAAAGATATAAATATGATAGCCA	3905
Db	301	ATCATCTAGCAAGAAGAAGTAGTAGAAGCACTGAGGAGGAAATACGAGTATAGTCA	360
OY	3906	TCTGATCATCCAAACATCATTAATAGATTTGGGACCCACAGCTGTGAGAGACATTTACA	3965
Db	361	TCTAAACATCTTAATATTAATTTGCGATTTGGGTGCTACATGTGAGAGAGACACTACAA	420

QY 3966 TCTCTTCATTGATGATGGCAGGGGATGCGCTCATTTGCTGAGTAATATGAGC 4025
|||||
Db 421 CCTCTTCATTGATGATGGCAGGGGATGCGCTCATTTGCTGAGTAATATGAGC 480
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QY 4026 CTTCAGAAATCAGTATGTTTAACTACACTGAACAGTTACTCGCTGCTTGTCT 4085
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Db 481 CTTCAGAAATCAGTATGTTTAACTACACTGAACAGTTACTCGCTTGTCTT 540
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QY 4086 CCATGAAAACCAATCATTCACAGAGATGTCMAAGGTGCAATTTGCTAAATGACAGC 4145
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Db 541 CCATGAGAAATCAGATTAATTCATAGAGATGTCMAAGGTGCAATTTGCTAAATGACAGC 600
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QY 4146 TGTCTGACAGACTAAGATTTGACATTTTGGAGCTGCACGCCAGTTGGCATCAAAAGAAC 4205
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Db 601 AGGTCTAGATGTTAAGATTTGCTGATTTTGGAGCTGCACGCCAGTTGGCATCAAAAGAAC 660
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QY 4206 TGTGTGAGAGAGATTTGACAGCAATTTACTGCGGACAAATTTGCTAAATGACAGC 4262
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Db 661 TGTGTGAGAGAGATTTGACAGCAATTTACTGCGGACAAATTTGCTAAATGACAGC 716
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RESULT 6
AM499603 530 bp mRNA linear EST 01-MAR-2000

LOCUS UI-HF-BP0P-ain-b-12-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone
DEFINITION IMAGE:3072335 5', mRNA sequence.

ACCESSION AM499603
VERSION AM499603.1 GI:7111428
KEYWORDS EST.

SOURCE ORGANISM

human.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NIH-MGC http://mhc.nci.nih.gov/
TITLE 1 (bases 1 to 530)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrr/image/image.html
Seq primer: M13 forward

FEATURES
source location/Qualifiers
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/clone="IMAGE:3072335"
/clone_1ib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LT1)"
/note="Vector: pT7T3-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 141 a 116 c 116 g 157 t

Query Match 9.9%; Score 519.8; DB 10; Length 530;
Best Local Similarity 99.6%; Pred. No. 8.7e-101;
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2268 TCTTGGCCGCGCTTGTCTTATAGATAGCTGTGTTGGAATTTCCCTGTAATTTATCC 2327
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Db 8 TCTTGGCCGCGCTTGTCTTATAGATAGCTGTGTTGGAATTTCCCTGTAATTTATCC 67
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QY 2328 TCATATTTGATGATGATGTTTTCACAGCTGAGCCTGTTGAATACGTTAAGAACT 2387
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Db 68 TCATATTTGATGATGATGTTTTCACAGCTGAGCCTGTTGAATACGTTAAGAACT 127
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QY 2388 GCTGTCCCTCTTAACTCTTCTTGGAGCTCCATTTGATTAATTTCCACATGTTGGCAA 2447
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Db 128 GCTGTCCCTCTTAACTCTTCTTGGAGCTCCATTTGATTAATTTCCACATGTTGGCAA 187
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QY 2448 ACTTTCAGAGAGATCTACTTGAAGTTGTCAGAGATGTTACTACAGTACCCATGTT 2507
|||||
Db 188 ACTTTCAGAGAGATCTACTTGAAGTTGTCAGAGATGTTACTACAGTACCCATGTT 247
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QY 2508 TTCAAAACCTTTAGAAATGCTGAGTGTTCACAGTTCCACTTCACAGAGATGCTGC 2567
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Db 248 TTCAAAACCTTTAGAAATGCTGAGTGTTCACAGTTCCACTTCACAGAGATGCTGC 307
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QY 2568 CCGTTTATGCTTATTTGACATGAGTGGAAATTTCCGGAAGCCATCCAGTTGGCGTGA 2627
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Db 308 CCGTTTATGCTTATTTGACATGAGTGGAAATTTCCGGAAGCCATCCAGTTGGCGTGA 367
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QY 2628 AGACACTTTGATGATGTCACAGAGACAGCTCTTTCAGAGCATCTGTTCCCAACATATCT 2687
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Db 368 AGACACTTTGATGATGTCACAGAGACAGCTCTTTCAGAGCATCTGTTCCCAACATATCT 427
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QY 2688 GGAACCCACAGAGAACAGTTCCCTGAGTGCACAGTCCATTAGAGAAACCTGGAAGG 2747
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Db 428 GGAACCCACAGAGAACAGTTCCCTGAGTGCACAGTCCATTAGAGAAACCTGGAAGG 487
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QY 2748 ATTTATGCTTACAAATTTGAGTGCCTTTCAGAGACATTTCT 2790
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Db 488 ATTTATGCTTACAAATTTGAGTGCCTTTCAGAGACATTTCT 530
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RESULT 7
B1656574

LOCUS B1656574 719 bp mRNA linear EST 12-SEP-2001
DEFINITION 603284924F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5329373 5',
mRNA sequence.

ACCESSION B1656574
VERSION B1656574.1 GI:15570810
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 719)
JOURNAL NIH-MGC http://mhc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1835 row: 0 column: 06
High quality sequence stop: 719.
location/Qualifiers
1..719

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Db 241 AACTGTGAAATGCTGAGTGTTCCTCAGTCCACTCCTCCAGCAGAGTGCCTGCTT 300
QY 2573 TGATGCTATTTGCAAGTGTGCAATTCGCCAAGCCATTCAGTGGCGCTAGAGACA 2632
Db 301 TGATGCTATTTGCAAGTGTGCAATTCGCCAAGCCATTCAGTGGCGCTAGAGACA 360
QY 2633 CTGTGATGGCAACAGACGCTTCTGAGGATCTGCTCCCAACAATCTGGA 2692
Db 361 CTGTGATGGCAACAGACGCTTCTGAGGATCTGCTCCCAACAATCTGGA 420
QY 2693 CCACAGAGAACAGTTCCTGAGTGCACAGTCTATTAGAGAAACTGGAAAA 2745
Db 421 CCACAGAGAACAGTTCCTGAGTGCACAGTCTATTAGAGAAACTGGAAAA 473

RESULT 15
AL135609 470 bp mRNA linear EST 25-FEB-2000
LOCUS DKE2P762P244_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
DEFINITION DKE2P762P244 5', mRNA sequence.
ACCESSION AL135609
VERSION AL135609.1 GI:6603796
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 470)
AUTHORS Koehler,K., Beyer,A., Mewes,W., Well,B. and Wiemann,S.
TITLE EST (Koehler,K., Beyer,A., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Koehler K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFZP762P244) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 148 a 87 c 94 g 141 t
ORIGIN
Query Match 9.0%; Score 470; DB 9; Length 470;
Best Local Similarity 100.0%; Pred. No. 4.2e-90;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4577 GGATGCTCAACAGAGAAAAAAGTGTGGGGAACCATGATTTCTAGTGGCCATG 4636
Db 1 GGATGCTCAACAGAGAAAAAAGTGTGGGGAACCATGATTTCTAGTGGCCATG 60
QY 4637 ATGCCACTGAACAGCTATGAAGAGGCCAGTGGGAACCTTACCTAAGTATGTGATGA 4696
Db 61 ATGCCACTGAACAGCTATGAAGAGGCCAGTGGGAACCTTACCTAAGTATGTGATGA 120
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QY 4697 CAATTCATGATCTGACTTAAGCTCAGTATGCAAAAGCCCAAACTAGTGAGAACTGTA 4756
Db 121 CAATTCATGATCTGACTTAAGCTCAGTATGCAAAAGCCCAAACTAGTGAGAACTGTA 180
QY 4757 AACTGTGCTTTCAAAAGACAGCGCCCTAGTGAACAGAGAAACAATGAAGTTGATGATAC 4816
Db 181 AACTGTGCTTTCAAAAGACAGCGCCCTAGTGAACAGAGAAACAATGAAGTTGATGATAC 240
QY 4817 TAAATTCAGAGACATATTTATTTTGTGAGACATTTTCAGCAATATTAGGGCTG 4876
Db 241 TAAATTCAGAGACATATTTATTTTGTGAGACATTTTCAGCAATATTAGGGCTG 300
QY 4877 AGGGGCTCAGATCTATTTTAATTTCAATTTCTTCATTTCTATAGTATGATCACA 4936
Db 301 AGGGGCTCAGATCTATTTTAATTTCAATTTCTTCATTTCTATAGTATGATCACA 360
QY 4937 GCAGGGGTTCTGCAATTCGTTCAAAATTTTGTGACGTGCTATTAATAGTATGTC 4996
Db 361 GCAGGGGTTCTGCAATTCGTTCAAAATTTTGTGACGTGCTATTAATAGTATGTC 420
QY 4997 CTCTTTAGTTCAGAGTATGCTATGATGATGAGCAATTCATATATTTT 5046
Db 421 CTCTTTAGTTCAGAGTATGCTATGATGATGAGCAATTCATATATTTT 470
```

Search completed: December 27, 2002, 22:14:55
Job time : 6281 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:45 ; Search time 60 Seconds

(without alignments)
5192.387 Million cell updates/sec

Title: US-09-697-898-2

Perfect score: 7825
Sequence: 1 MAAAGNRRASSSGFPGARAT.....PODRPSELKHPVFRITW 1512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_minc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595.5	7.6	690	10 Q40541	Q40541 nicotiana t
2	595.5	7.6	1230	3 Q9HFT9	Q9HFT9 cryptococcu
3	591.5	7.6	651	10 Q9F236	Q9F236 arabidopsis
4	587.5	7.5	642	10 Q22041	Q22041 arabidopsis
5	578	7.4	651	10 Q22042	Q22042 arabidopsis
6	576.5	7.4	585	10 Q9C7M0	Q9C7M0 arabidopsis
7	576	7.4	376	10 Q22040	Q22040 arabidopsis
8	576	7.4	661	10 Q22039	Q22039 arabidopsis
9	562.5	7.2	942	5 Q96611	Q96611 dictyostell
10	558.5	7.1	591	10 Q82667	Q82667 brassica na
11	557.5	7.1	594	4 Q96H89	Q96H89 homo sapien
12	552.5	6.9	1338	3 Q60030	Q60030 kluyveromyc
13	542	6.9	666	3 Q42625	Q42625 neurospora
14	539.5	6.9	619	4 Q9NYK3	Q9NYK3 homo sapien
15	538.5	6.9	883	10 Q9CAD5	Q9CAD5 arabidopsis
16	536.5	6.9	609	10 Q8W582	Q8W582 arabidopsis

17	531.5	6.8	608	10 Q9LPH2	Q9LPH2 arabidopsis
18	531	6.8	608	10 Q9ZRF7	Q9ZRF7 arabidopsis
19	531	6.8	608	10 Q9LIM7	Q9LIM7 oryza sativ
20	531	6.8	1166	3 Q9P4E0	Q9P4E0 ustilago ma
21	523	6.7	823	3 Q9HFR3	Q9HFR3 pneumocysti
22	521.5	6.7	1832	3 Q8TGH8	Q8TGH8 podosporea
23	484	6.2	652	10 Q04030	Q04030 arabidopsis
24	483	6.2	582	10 Q82649	Q82649 arabidopsis
25	480	6.1	716	10 Q9C5H5	Q9C5H5 arabidopsis
26	479	6.1	716	10 Q932H4	Q932H4 arabidopsis
27	477	6.1	1612	5 Q9VE37	Q9VE37 drosophila
28	473	6.0	1497	5 Q95YH6	Q95YH6 drosophila
29	473	6.0	1571	5 Q95YH7	Q95YH7 drosophila
30	472	6.0	847	10 Q8W5G2	Q8W5G2 oryza sativ
31	467.5	6.0	608	10 Q8W4N5	Q8W4N5 arabidopsis
32	461.5	5.9	608	10 Q39020	Q39020 arabidopsis
33	461.5	5.9	608	10 Q81470	Q81470 arabidopsis
34	455.5	5.8	650	5 Q24458	Q24458 drosophila
35	455.5	5.8	1310	5 Q9VDS9	Q9VDS9 drosophila
36	449.5	5.7	376	10 Q9FKZ5	Q9FKZ5 arabidopsis
37	449.5	5.7	535	10 Q82650	Q82650 arabidopsis
38	447	5.7	773	10 Q81472	Q81472 arabidopsis
39	446	5.7	372	10 Q23721	Q23721 arabidopsis
40	445.5	5.7	560	10 Q9W0T3	Q9W0T3 arabidopsis
41	443.5	5.7	1289	11 Q9WTR2	Q9WTR2 mus musculu
42	442.5	5.7	1368	10 Q81809	Q81809 arabidopsis
43	441.5	5.6	1368	10 Q9LJD8	Q9LJD8 arabidopsis
44	439	5.6	575	10 Q82668	Q82668 brassica na
45	437.5	5.6	1299	10 Q9STED	Q9STED brassica na

ALIGNMENTS

RESULT 1

Q40541 PRELIMINARY; PRT; 690 AA.
ID Q40541
AC Q40541;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Protein kinase.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Machida Y.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9330268; PubMed=8336712;
RA Banno H., Hirano K., Nakamura T., Irie K., Nomoto S., Matsumoto K.,
RA Machida Y.;
RT "NPK1, a tobacco gene that encodes a protein with a domain homologous
to yeast BCK1, STE11, and Byr2 protein kinases.";
RL Mol. Cell. Biol. 13:4745-4752(1993).
CC -!- SIMILARITY: BELONGS TO THE SHR/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D26601; BA05648.1; -!
DR HSSP; P24941; IAO1.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR002290; Ser_thr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Euk_Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SO SEQUENCE 690 AA; 76241 MW; 2F9C2A3A31C6094 CMC64;


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Db 1054 NYLHMRGIVYHRTDKGANILVDNKG-GIKISDFGISKVENSLLTGTNTNPSLOGSVFW 1112
OY 1417 APEVLGGOYGRSCDVSVCALIIEMACAKPPNNAEKSHNLAIFFKIASATTAPISPH 1476
Db 1113 APEVYKOTSYSPRADIMSVGCLVEMLTGTHPM---ADLTQMAIFRIGS-LARPAPSD 1168
OY 1477 LSPGLRDVALRCLELOPPDRPPSRELLKHP 1506
Db 1169 ISVOADEFLKTFEIEHAKRPFAQLKHP 1198

RESULT 3
OY 09F236 PRELIMINARY; PRT; 651 AA.
AC 09F236;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE NPk1-related protein kinase 2.
GN T24C10.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federici P.M., Palm C.J., Conway A.B., Comp L., Hansen N.F.,
RA Altieri H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buelher E., Chao Q., Chin C., Chlou J., Choi E., Gonzalez A.,
RA Hough B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
RA Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC064840; MAG00876.1;
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 651 AA; 71848 MW; 0204655E1F9E918E CRC64;

Query Match 7.6%; Score 591.5; DB 10; Length 651;
Best Local Similarity 43.3%; Pred. No. 2.9e-28;
Matches 119; Conservative 55; Mismatches 90; Indels 11; Gaps 5;

OY 1234 KOPYREDTEMLKGOIGLGFSSCYQADVGTGLMAVKQVTVYRNTSSQ--EEVEAL 1291
Db 63 KPPIR---WRKQGLIGRGAFGYVMGMNDSCGELLAVKQVLTLSNCASEKTKQAHIQEL 118
OY 1292 REIRBMASHLNHPNITRMIGATCEKSNYNLFIEWMAGGSVAHLISKGAKRESVINYTE 1351
Db 119 EEEVKLLKKNLSHPNIVYLTGTVREDETLNITLLEFVPGSSISLLEKFGAPESVVRYYTN 178
OY 1352 QLLRGSLYLHENQIIHRDVGANLLIDSTGQRLRIADFGAARLASGTGAGEFQGLG 1411
Db 179 QLLGLELYLNHAIHMHDIGANILVDNKG-CIKLADFGASKOVAELATISG--AKSMKG 235
OY 1412 TIAPMAPEVLKGOYGRSCDVSVCALIIEMACAKPPNNAEKSHNLAIFFKIASATTAP 1471
Db 236 TTYWMAPEVILQTHGSHFSADIMSVGCTVIEWYTGKAPWS--QQYKEIAIIFHIGTKSHP 293
OY 1472 SIPSHLSPGLRDVALRCLELOPPDRPPSRELLKHP 1506
Db 1472 SIPSHLSPGLRDVALRCLELOPPDRPPSRELLKHP 1506
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Db 294 PIPDNISSDANDELLKCLQOEPPNLRPTASLELLKHP 328

RESULT 4
OY 022041 PRELIMINARY; PRT; 642 AA.
AC 022041;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NPk1-related protein kinase 2 (Fragment).
GN AMP2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-COL-0;
RA MEDLINE-97408932; PubMed=9263451;
RA Nishihara R., Hano H., Kawahara E., Irie K., Machida Y.;
RT "Possible involvement of differential splicing in regulation of the
RT activity of Arabidopsis AMP1 that is related to mitogen-activated
RT protein kinase kinase kinases (MAPKKKs).";
RT Plant J. 12:39-48(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB000798; BAA21856.1;
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Kinase; Serine/threonine-protein kinase.
FW NON_TER 1
SQ SEQUENCE 642 AA; 70786 MW; C277182DD79002E3 CRC64;

Query Match 7.5%; Score 587.5; DB 10; Length 642;
Best Local Similarity 42.9%; Pred. No. 4.9e-28;
Matches 118; Conservative 55; Mismatches 91; Indels 11; Gaps 5;

OY 1234 KOPYREDTEMLKGOIGLGFSSCYQADVGTGLMAVKQVTVYRNTSSQ--EEVEAL 1291
Db 54 KPPIR---WRKQGLIGRGAFGYVMGMNDSCGELLAVKQALITLSNCASEKTKQAHIQEL 109
OY 1292 REIRBMASHLNHPNITRMIGATCEKSNYNLFIEWMAGGSVAHLISKGAKRESVINYTE 1351
Db 110 EEEVKLLKKNLSHPNIVYLTGTVREDETLNITLLEFVPGSSISLLEKFGAPESVVRYYTN 169
OY 1352 QLLRGSLYLHENQIIHRDVGANLLIDSTGQRLRIADFGAARLASGTGAGEFQGLG 1411
Db 170 QLLGLELYLNHAIHMHDIGANILVDNKG-CIKLADFGASKOVAELATISG--AKSMKG 226
OY 1412 TIAPMAPEVLKGOYGRSCDVSVCALIIEMACAKPPNNAEKSHNLAIFFKIASATTAP 1471
Db 227 TTYWMAPEVILQTHGSHFSADIMSVGCTVIEWYTGKAPWS--QQYKEIAIIFHIGTKSHP 284
OY 1472 SIPSHLSPGLRDVALRCLELOPPDRPPSRELLKHP 1506
Db 285 PIPDNISSDANDELLKCLQOEPPNLRPTASLELLKHP 319

RESULT 5
OY 022042 PRELIMINARY; PRT; 651 AA.
AC 022042;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
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DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE NP1-related protein kinase 3 (Atg3g0630/F24F17_1).
 GN ANP3 OR F24F17.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COL-0;
 RX MEDLINE=974089332; PubMed=9263451;
 RA Nishihama R., Banno H., Kawahara E., Irie K., Machida Y.;
 RT "Possible involvement of differential splicing in regulation of the
 RT activity of Arabidopsis ANP1 that is related to mitogen-activated
 RT protein kinase kinase kinases (MAPKKKs).";
 RL Plant J. 12:39-48(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 RA Matli R., Rongning C.M., Koo H., Fujii C.Y., Uterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC F24F17 genomic sequence.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
 RA Carinici P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Islida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB000799; BA021857.1; -;
 DR EMBL; AC068073; AA06131.1; -;
 DR EMBL; AY069917; AL04745.1; -;
 DR HSSP; P24941; IAO1.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 651 AA; 71654 MW; E8FD683C7E31268 CRC64;
 Query Match 7.4%; Score 578; DB 10; Length 651;
 Best Local Similarity 40.7%; Pred. No. 2e-27;
 Matches 116; Conservative 57; Mismatches 102; Indels 10; Gaps 5;
 QY 1224 PETLPGRKAKQPYRDETEWLKGGQIGLGFSSCYQAOVDGTGTLMAVKQYTVYNTSSQ 1283
 DB 52 PPGJPAPEKKEP---SIRMRKGLICGAFGRVYMGNNLDSGELLAKQVLIAPSSAK 108
 QY 1284 QEEV--VERALREETRMHSHLNHPNIIIRMLGATCEKSNYNLFTEMAAGSVANLLSKYAF 1341
 DB 109 EKTQGHILELEEVOLLNLNLSHPNIVRLGTVRESDSLNIILEFVPGGISISLEKFGSF 168
 QY 1342 KESVINTEQDLRLGLSYLHENQIIRDPVKANLLIDSTGQRLRIADGGAARLASKSTG 1401
 DB 169 PEVYIMTKQLLGLLEVLHNGIMHRDIKAGNIIYDNGK-CIRIADGASAKVVELATV 227
 QY 1402 AGEFQGLLTATAPARVLRGQDGRSCDVYSGCAITTEMACAKPWNNAEKHSHNLALI 1461
 DB 228 NG--AKSMKGPRYMAAPRVIILQTHSGFSADIMSVGCTVIEMATGKPPMS--EQYQGFNAV 283

QY 1462 FKIASATTTPSPSHSPGLRYVALRCLELPQDPRPSPELLKHP 1506
 DB 284 LHIIGTRKAPHPEDLSPEAKDFIMKCLKKEPSRLSATTELLQHP 328
 RESULT 6
 QY 09C7M0 PRELIMINARY; PRT; 585 AA.
 AC 09C7M0;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DE NP1-related protein kinase, putative.
 GN P14C21.49.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehlner E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luyos J.S., Matli R., Marzilli A.,
 RA Miltsher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).
 DR EMBL; AC069144; AAG51109.1; -;
 DR HSSP; P24941; IAO1.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 585 AA; 64716 MW; E8AC66F2452A0166 CRC64;
 Query Match 7.4%; Score 576.5; DB 10; Length 585;
 Best Local Similarity 42.9%; Pred. No. 2.1e-27;
 Matches 117; Conservative 55; Mismatches 90; Indels 11; Gaps 5;
 QY 1224 KQPYRDETEWLKGGQIGLGFSSCYQAOVDGTGTLMAVKQYTVYNTSSQ--EEVEAL 1291
 DB 63 KPPIR---WRKQGLIGRGAFTYVYMGNNLDSGELLAKQVLIITNSCAKSKETQAHIGEL 118
 QY 1292 REEIRMSHNLNHPNIIIRMLGATCEKSNYNLFTEMAAGSVANLLSKYAFKESVYINTE 1351
 DB 119 EEEVRLNLNLSHPNIVRLGTVREDETNIILEFVPGGISISLEKFGAFESVVRVTYN 178
 QY 1352 QLLRLSYLHENQIIRDPVKANLLIDSTGQRLRIADGGAARLASKSTGGEFGQLG 1411
 DB 179 QLLGLLEVLHNLHAIHRDIKAGNIIYDNGK-CIRIADGASAKVVELATISG--AKSMKG 235

QY	1412	TAFAPAFVLTGGOQGRSCDWSVCCATITEMACAPPMNAEKHSNHLAIFFIATATAP	1471
Db	236	TPYKMAPEVILQGTGSEFADIMSVCCYIVTEWYTGAPMS--QGYKEIAAIFHIGTTKSHP	293
QY	1472	SIPSHLSPGLRDVALRCLELPQDRPSPRELLK	1504
Db	294	PIDPSSDANDFLKCIQOEPLNRPTASELLK	326
RESULT 7			
ID	022040	PRELIMINARY;	PRT; 376 AA.
AC	022040;		
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-JAN-1998	(TREMBLrel. 05, last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, last annotation update)	
DE		NPFL-related protein kinase 1S.	
GN	ANP1.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eustoids II; Brassicales; Brassicaceae; Arabidopses.		
OX	NCBI_Taxid=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=COL-0;		
RX	MEDLINE=97408932; PubMed=9263451;		
RA	Nishihama R., Banno H., Kawahara E., Irie K., Machida Y.;		
RT	"Possible involvement of differential splicing in regulation of the		
RT	activity of Arabidopsis ANP1 that is related to mitogen-activated		
RT	protein kinase kinase kinases (MAPKKs).";		
RL	Plant J. 12:39-48(1997).		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL; AB000797; BAA21855.1; -.		
DR	HSSP; P24941; IAO1.		
DR	InterPro; IPR000719; Euk_Pkinase.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	Prodom; PD000001; Euk_Pkinase; 1.		
DR	SMART; SM00220; S_TKC; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.		
SO	SEQUENCE 376 AA; 41384 MW; P23B085218673456 CRC64;		
Query Match		7.4%; Score 576; DB 10; Length 376;	
Best Local Similarity		42.3%; Pred. No. 1.le-27;	
Matches 119; Conservative 53; Mismatches 99; Indels 10; Gaps 5;			
QY	1228	PGHFKAKPYREDPTFMKGGQIGIGAFSSCYAQDVGCTIMAKVQYVYRTTSSEQ--E	1285
Db	57	PANVTADNP---PISWRGQLIGAFGFTVYGMNIDSELLAVQVLTAAVPAKREKTO	113
QY	1286	EVEVALREIRIMSMHNPILITRMIGALCEKSNYMLIETMMAGGSVAHLISYKAFKESV	1345
Db	114	AHIOGLEEVVLTAKMLKLSHPNIVRYIGTVAREDDTLNMLEFVGGSSISLLEKFGPPPEV	173
QY	1346	VINTTEOLLRLGLSYHENQIITHRDYKANLLIDSTGQRLTIADFGAARLASKGTGAGEV	1405
Db	174	VRTYRQLLLGLEEYLNHNAIMHRDIKGANIITDNGK-CIKLADFGASKOVAELATMTG--	230
QY	1406	OGOLGTLAFAPEVLRCGOQGRSCDWSVCCATITEMACAPPMNAEKHSNHLAIFKTA	1465
Db	231	AKSMGIYMAAPEVILQGTGSEFADIMSVCCYIVTEWYTGAPMS--QGYKEVAAIFFTG	288
QY	1466	SATPAPISPSHLSPGLRDVALRCLELPQDRPSPRELLKHP	1506
Db	289	TTKSHPIPDLTSSDAKDFLKCIOEYVNLRTPTASELLKHP	329
RESULT 8			

ID	Q22039	PRELIMINARY:	PRT:	661 AA.
AC	Q22039:			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	NPk1-related protein kinase 1L (fragment).			
GN	ANP1.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COL-0;			
RX	MEDLINE=97408932; PubMed=9263451;			
RA	Nishihama K., Banno H., Kawahara E., Irie K., Machida Y.;			
RT	"Possible involvement of differential splicing in regulation of the			
RT	activity of Arabidopsis ANP1 that is related to mitogen-activated			
RT	protein kinase kinase kinases (MAPKKs).";			
RL	Plant J. 12:39-48(1997)."			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	EMBL, AB000796; BAA21854.1; -.			
DR	HSSP; P24941; IAO1.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_thr_pkinase.			
DR	InterPro: IPR001245; Tyr_pkinase.			
DR	Pfam: PF00069; pkinase; 1			
DR	PRINTS: PR00109; TYRKINASE.			
DR	ProDom: PD000001; Euk_pkinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	kinase; Serine/threonine-protein kinase.			
FT	NON_TER			
SO	SEQUENCE 661 AA; 72801 MW; 3A5E83BCFEDE18A1 CRC64;			
Query Match 7.4%; Score 576; DB 10; Length 661;				
Best Local Similarity 42.3%; Pred. No. 2,7e-27;				
Matches 119; Conservative 53; Mismatches 99; Indels 10; Gaps 5				
QY	1228 PCHTAKQDPREDTEMLKQOIGLGFSSCYQADYGTGTMAVKQVYRNTSSQ--E	1285		
DB	52 PANTYDMPA--PISWRKQOLIGRGAFGVYGMNDSGELLAVKQVLLAANFAASKETQ	108		
QY	1286 EVEVLAERIRKMSHLNHNIRIMGATCEKSNYNLFIMMAGGSVAHLISYGAFKESV	1345		
DB	109 AHIOGLEEVKLIKLNLSHNPIRYRIGYVAEDDTLLNLEFVGGSISLLEKFGPPESV	168		
QY	1346 VINTYEQLLRGLSYLAENQIIRHDYKGANLLIDSTGQRLIADFGAARIASKTGACGF	1405		
DB	1469 VETTYRQLLIGLEYLHNHIMHRDIKGANILVDNKG--CIKLDFGASKVDELATWTG--	225		
QY	1406 OGQLLGTAFAFMEVLRGGQYGRSDWVGCAIIEIMACAKPPMAEKISNHLALFKTA	1465		
DB	226 AKSMGSGTYWMAPEVILQTHGFSFADIMVSGCTVLEMTVGKAPWS--QDYKEVAALFTG	283		
QY	1466 SATTAPISPSLGLRDVALCLLELOPQDPRPSRELLKHP	1506		
DB	284 TTKSHPIPDLTSSDAKQELKLCLEQVPLRLRTASBLKHP	324		
RESULT 9				
ID	Q96611	PRELIMINARY:	PRT:	942 AA.
AC	Q96611:			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	MEK kinase alpha.			
GN	MKKA.			

OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KAX-3;
RX MEDLINE=99051319; PubMed=9832508;
RA Chung C.Y., Keddy T.B.K., Zhou K., Firtel R.A.;
RT "A novel, putative MEK kinase controls developmental timing and
spatial patterning in Dictyostelium and is regulated by ubiquitin-
mediated protein degradation.";
RL Genes Dev. 12:3564-3578(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF093689; AAC97114.1; -.
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR000270; Octrept_molif.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00069; kinase; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR PRODOM: PD00018; WD40; 1.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00016; OPR; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_4.
DR PROSITE: PS50082; WD_REPEATS_2; 5.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR ATP-binding; kinase; Repeat; Serine/threonine-protein kinase;
KW Transferase; WD repeat.
SQ SEQUENCE 942 AA; 105796 MW; C9E4928A8C7C68F7 CRC64;

Query Match 7.2%; Score 562.5; DB 5; Length 942;
Best Local Similarity 38.4%; Pred. No. 3.1e-26;
Matches 119; Conservative 65; Mismatches 89; Indels 37; Gaps 7;

OY 1212 NGEDIIIIQQOQTP-----ETLGHHTKAKQPYREDTEWKLGGQIIGLGAFFSSCYQADYV 1263
DB 140 NNNNTIIGHTDPSPILINHEHELISN-----NIRWGGQILRGYGSVYLGLNK 190
OY 1264 GTGLTAAVKQVTVYR-NTSSEQEEVEALREIRRMASHLNPIITRMGATCEKSNYNLF 1322
DB 191 DTGELFANQLEIVDINDPKAKNMILSFSKEIEMRSIRHDNIYRYLTSLDQFLSYF 250
OY 1333 IEMWAGGSVAHLISKYGAFFKESVINTYEQLLGLSTYLHENQIIRHDYGANLLIDSTGQ 1382
DB 251 LEYIGGSISSLGKFGAFSENVIVYTKQILOGSLFLHANSIIRHDIKGANILLDTKG- 309
OY 1393 RLRIIDFGAARALASKGAGGAFGQ-----QLLGTIAFMAPEVLRGQOYGSCVWSWG 1436
DB 310 IVKLSDFECSK-----SFGSIVQSFKSMOQTPYMAAEVIRKQGHGSSDIWSIG 359
OY 1437 CAIEMACAPPMWAEKSHNLALIFKIASATTAPISPHLSPGLRDVALRCLTELOPOR 1496
DB 360 CVIYEMATAQPPWS--NTTELLAAVYVHTIASSNSINIPSHMSQGEAFDPLNLCFKDPKER 417
OY 1497 PPSRELLKHP 1506
DB 418 PDANOLLKHP 427

RESULT 10
082667 ID 082667 PRELIMINARY; PRT; 591 AA.
AC 082667;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MAP3K alpha 1 protein kinase (EC 2.7.1.37).
GN MAP3K ALPHA 1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, TOPAS;
RX MEDLINE=99196996; PubMed=10095117;
RA Jounanin S., Hamal A., Leprince A.S., Tregear J.W., Kreis M.,
RA Henry Y.;
RT "Characterisation of novel plant genes encoding MEKK/STE11 and RAF-
related protein kinases.";
RL Gene 229:171-181(1999).
DR EMBL: AJ010091; CAA08995.1; -.
DR HSSP: P24941; 1CKP.
DR InterPro: IPR00719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; kinase; 1.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; kinase; Transferase.
SQ SEQUENCE 591 AA; 64507 MW; EAFAC591708C1FC8 CRC64;

Query Match 7.1%; Score 558.5; DB 10; Length 591;
Best Local Similarity 29.3%; Pred. No. 2.7e-26;
Matches 149; Conservative 83; Mismatches 190; Indels 87; Gaps 14;

OY 1031 RNCPNKDSDKLSPVETOSRPLPSSNIHHRKPSRPTPGNTSKQGPSKSNWTLIDNSSK 1090
DB 7 RKSXKNDSHL--LQYQTRSVSDKSIR-----RISADNSKSSPPVYPS-----RCTPR 54
OY 1091 CDDSGFGSSNSSNAVIIPSDIEVTFPEEKCRLDY---NTELNSSIEDLLEASMP-- 1142
DB 55 CSREFAGASGFED-----EKKCHPLPLPSLNDQVNSVSGSGSVSSVSSG 101
OY 1143 -----SDTYTFKSEVAYLSPEKA-----ENDDYTKDDVINNOCKEKEM 1181
DB 102 SGEQDSQPTAPRKSNAAPKAGARPTSPILNRRSGMTLESSYGRDNDGR----- 153
OY 1182 EAEEREAALIAMASASODALPIVPOLOVNGEDIIIIQQOQTPETLPGHTKAKQPYREDT 1241
DB 154 -----SSEIHRLPLPPGSPSPSVVLPCEPTSSSGVQGSWVVGSEKELS 199
OY 1242 EWLKQOQIGLGAFFSSCYQADYGTGLTAAVKQVTVYRNTSSQEEVEALREIRRMASHL 1301
DB 200 KWKRCRFISGTFGKYVQGFNSEEGRICAKKEVYI-SDDKSKRCLKQLOINQEIIVLSQL 258
OY 1302 NHPNIIIRMGATCEKSNYNLFIEWAGGSVAHLISKYGAFFKESVINTYEQLLGLSTYLH 1361
DB 259 GHPNIVQYQYSELSSETLSVLEFVSGSIXKLLTEYGAFTPEVIONYTRQIYGLAYLH 318
OY 1362 ENQIIRHDYKANLLIDSTGQRLRIADFGAARALASKGAGGAFGQGLLGTIAFMAPEVL 1421
DB 319 GRNIVYHRDIKGANILLVDNGE-ITLADFGMAKHVTAYST-----MLSTGSGPYMAPEVY 372

QY 1422 RG00-YRSCDVMVSGCAIIEMACAPPMNAEKSHNLALIFKATATAPISPSHSPG 1480
DB 373 MRRKGYTLADVMSVSGCTIEMATAPKPPWS--OPEGVAALFKIGNSKDMEIDHLSL 429
QY 1481 LRVALRCLLEPODRPSEKLLKHPYER 1509
DB 430 AKNFIKCLQNRNPRVPRTAQDLEHPELR 458
RESULT 11
096HN9 PRELIMINARY; PRT: 594 AA.
AC 096HN9; 19, Created
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:3506235) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC008336; AA08336.1;
DR InterPro: IPR000719; Euk_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
FT NON_TER 1
SQ SEQUENCE 594 AA; 67092 MW; P493865DB2F8C3D CRC64;
Query Match 7.1%; Score 557.5; DB 4; Length 594;
Best Local Similarity 31.4%; Pred. No. 3.2e-26;
Matches 161; Conservative 78; Mismatches 173; Indels 101; Gaps 20;
QY 1044 PVFTQSRPLPSSNIRKPKSPRPG-----NTSKOGDPSKNSMTLDLSSSKCDDSPFG 1096
DB 125 PPRSRHLSVSS-QNPGRSSPPGYVERQNHAROG-----SYT----- 164
QY 1097 CSSSSNAVIPSDETTPPEBEKRLDYNTLNSIEDLEASPPSSDTTY---TFKSEV 1153
DB 165 -SINSEGEIPE-----TSEQCLDP-----LSAENSLSGSCOSIDRSADSPFSRSR 212
QY 1154 AVISPEKAENDDTYKD-----DYNHNOCKEKEAEEREE 1167
DB 213 MSRAQSPDRROEYSDKETQLDKGVAGGTYPRRYHVSMMHKDYSQGRTPRIRRHQGN 272
QY 1188 ALAI--AMAMASQDALPIVPO-----LQVNGEDIIITQDTPETLLPGHTKAPQY 1237
DB 273 LFTLVPSRSRLSTNGEMGLAVQYLDPRGRLSADSEMAISVGERNNPT-----KSP- 324
QY 1238 REDTEMLKGOQIGAGSSCQADQVGTGTLMAVKQYTYANTSSQDEVEYEALEETIRM 1297
DB 325 SAPINMRGKLLGGAGAGRYVLCYDVTGRELASKQVQFPDP-SPEFSKEVSALECEIOL 383
QY 1298 MSHLNHNIRIIMLGATGECSENYNL--FLEWMAAGSVAHLISKYAPFESVYINTEOLLR 1355
DB 384 LKNQHERIYQYVGLADRAEKTITIMEYVPGSSVKDQLKAYCALRESYTRKTTROTLE 443
QY 1356 GLSLYHNGIIRHDYKANLLIDSTGQRLIADFGAARLAS---KGTGAEFGOGOLIGT 1412
DB 444 GMSYLSHNMIVHRDIKANILRDSAG--NVKLGDEGASKRLQITCMGSG---MRSVGT 498
QY 1413 IAFAPAVLGGQVGRSCDVMVSGCAIIEMACAPPMNAEKSHNLALIFKATATAPIS 1472
DB 499 PYMSPSPVIGEGYGRADVMSLCTVEMTEKPPW-AEVEA--MAAFIKIAIQPTNPQ 555
QY 1473 IPSHLSPGLRDVALRCLLEPODRPSEKLLK 1505
DB 556 LPSHISEHGRDF-LRRTFVEARQRPASBELLIH 587

RESULT 12
060030 PRELIMINARY; PRT: 1338 AA.
AC 060030; 07, Created
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MAP kinase kinase kinase.
GN BCKL.
OS Kluyveromyces lactic (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_Taxid=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS2359/152;
RX MEDLINE=99262846; PubMed=10329146;
RA Jacoby J.J., Kirchath L., Gengenbacher U., Heinisch J.J.;
RT "Characterization of KIBCK1, encoding a MAP kinase kinase of
Kluyveromyces lacticus".
RL J. Mol. Biol. 288:337-352(1999).
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AJ005079; CA006336.1;
DR HSSP: P24941; IHCL.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR000719; Euk_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1338 AA; 148047 MW; BA86B15EB7122B5 CRC64;
Query Match 7.1%; Score 552.5; DB 3; Length 1338;
Best Local Similarity 25.0%; Pred. No. 2.2e-25;
Matches 211; Conservative 149; Mismatches 338; Indels 147; Gaps 32;
QY 741 ILGNQTESNMQELGRLCLID-----RLLEFPAPFYPIVSTDV-----SQAEVE 788
DB 535 VKSNASASANGEGSSDLTIDQGSRRRAVPQPSHYLYNSAEDVMSFDSVET 594
QY 789 IRYKLLSLTFAQSIDNSHSMYGLSRRIYLSARAVTVPIVFSK-LLEMLSVSSST 847
DB 595 IS-----DAPHITLPKSRPSLKLNSVLT---HASEKSTPRIITROTSDT 636
QY 848 HFTMRRLMAIADEVEIAEAIOLGVEDTLDGQDSFIQAVPNNYLETENSSPECTVH 907
DB 637 DIDNRKRRESFYVAELAPK-RKAPKPPVNG--NPVTSGSLPSAAMNVSESPLESPK 693
QY 908 LEKTKGKL-----CATKLSA-----SSEDSERIASISVGPSSSTTTTTTTT 949
DB 694 LDRNGKTIYQKNRPPLPTEFTERRSRSVSLSGQDLNE---VKESPVGSTFPASQV 749
QY 950 EQPKP---MQTGRPIISQCLNSSP-----LSHSQLMFPAISLP-----SSSTPS 992
DB 750 MYPQPKALTELLPKRSSADLSIRPMSLRQFSKNSLSLRKYLSTSRQTLNRTNSKPL 809
QY 993 VPAGTATVSKHRIQGFICRLIPSPASPTQKRFSLQFHRNQPENKDSKLSLSP-----VFT 1047
DB 810 VTSSTADIDPENDISF-----ADAPELSDSDDYSAASDEIIVS 848
QY 1048 QSRPLPSSNIRKPKSPRTPGNTSKQGPSKNSMTLDLSSSKCDDSPGSCSSNSN--- 1103
DB 849 RDRKISINDV---PEFSFTED-----TIDLVGDTTOVSGVATGEGSDTPKKM 893
QY 1104 AVISDEVEITPVEKCRLDVNTLNSIEDLEASPPSSDTTYTFKSEVAVLSPEKAEN 1163

DB 894 ALRPSDYYVYQNL-EKFFPDADLD-NPILGLTPPSNPADSSPSPRGFEKSLTKKSFQ 951
QY 1164 DTFYKDVVHNHOK---CEKMEAEERLALAMANSASODALPIVQ-LQVEN---GE 1214
DB 952 OPATLSRGSSQFLTPVSKLPKRTKTIRI-IAQEAERKNEVSKLQKRNKTMKGT 1010
QY 1215 DIIIIQDPTPELLPGHTKAKOPYREDETEWLKGGQIGLGFSSCYQADYGTGLMAVKQY 1274
DB 1011 KVEETIDKFTTISINSRNRSRGEYKE-FAMIKETIGKSGFGAYIALNVTTCGMLAVKQY 1069
QY 1275 TVVRNTSSQOE---EVEVALREERIMSHLNHPNIIIRMLGANCEKSNVLEFIEMAGSGV 1331
DB 1070 T-VPESSQDESAISMVNAKSEVSTLKDNLNHNITQYIGFEKKNITSLFLEYAGSGV 1128
QY 1332 AHLKRYGAFKSSVIVNTEQLRGSLSYLHENOIIHRDVGANLLIDSTGQRLIADFGA 1391
DB 1129 GSLIRMYGRFPDQILRHLYKQYLEGLAYLHSGCILHRDKMADNLIDNDGV-CKISDFGI 1187
QY 1392 AARLASKGAGGEPQQLGTLAFMAPEVL-RGQYGRSCDVWSVGCALIEMACAPPMN 1450
DB 1188 SKRSNNITYSNS---DPTMGTVFWMAPEMVDAHGSYSAKVDTWSLGCYVLEMPAGRRPWS 1244
QY 1451 AEKSHNHLALIEKIASATTAPSIPIH---LSPGLRDVALRCLQLQDPRPSELKHP 1506
DB 1245 ---NPEVNAAMFQIGKSKTAPPTPDTRKLVSPAGSGFLDQCFEIDPEMRPTASLVGHP 1301
QY 1507 VERTT 1511
DB 1302 FCKTS 1306

RESULT 13
ID 042625 PRELIMINARY; PRT; 666 AA.
AC 042625;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE MAPK kinase.
GN NRC-1.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98250677; PubMed=9584090;
RA Kothe G.O., Free S.U.;
RT "The isolation and characterization of nrc-1 and nrc-2, two genes
RT encoding protein kinases that control growth and development in
RT neurospora crassa."
RL Genetics 149:117-130(1998).
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF034090; AAC21676.1; -.
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000159; RA_domain.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 666 AA; 73634 MW; 2BCDFCF4B980DB1F CRC64;

Query Match 6.9%; Score 542; DB 3; Length 666;
Best Local Similarity 28.6%; Pred. No. 3.4e-25;
Matches 166; Conservative 92; Mismatches 215; Indels 108; Gaps 23;
QY 1013 RIPSASP---QYQKRFSL-----QFHRNCPENKXSDK----- 1041
|:| | | : | : | : | | | | | | | |

DB 99 RVPSGPGAELEERAAALIMEEAQOTHR--PRIPESDKKSQKLQKLVYGVGMDLQOQPP 156
QY 1042 LSPVFTQSRPLPSSN---IHRKP---SRPTGNTSKQD-----PSKNSMTLDLNSS 1089
DB 157 LSPMSYQDERBRNVNSAARDLERAPLETFRAMPRTQALRGQGLPSELIALSDLTSTV- 215
QY 1090 KCDSDSGCSSNSNNAVPEDEYFTVEKCHLD-VNTLNL-----SSIEDLEASM 1140
DB 216 -----PPDHSREAI---DRTARLSMRARSARLSRVNHLISVASTLSFASISID--APPI 263
QY 1141 PS-SDTTFVFKSEVAALISPEKA--ENDDTYKDDOVNH---NOKCEKMEAEERLALAMA 1194
DB 264 PTIADSWILASNOIAKVARRDVLPRAPIHGRSVASSVYDTIQEBSGSPTEPNRRSVPS 323
QY 1195 MSASODALPIV--POLQV-----ENGEIITIQDPTPELLPGHTKAKOPYR--- 1238
DB 324 DSGSDTAAVASVIDPDGNIIVRHSYSGTNMSDASVIOEALAE--DGEADAQKEIQTFLA 381
QY 1239 ---EPTENLKQOQIGLGFSSCYQADYGTGLMAVKQYTV-----RNTSDEEYVE 1289
DB 382 GDAMDSDMMKKSGLIGQSGFGSYLALHAITGELLAVKQVETPAPGADSKNDARKSKMTE 441
QY 1290 ALREERIMSHLNHPNIIIRMLGATCEKSNVNFIEWMAGSVAAHLISKYAKRESYVINY 1349
DB 442 ALKREITTLRDLOHPNITVYIGCSSAEYLNIFLEYPGSGVQTMDDYQALPESLVRSE 501
QY 1350 TEOQLRGSLSYLHENOIIHRDVGANLLIDSTGQRLIADFGAARLAS---KGTGACGF 1405
DB 502 VHQILOGSLYVNHRIIDHDIKGANILVDNKG-TIKISDFGJSKKEALINILGANNNH 560
QY 1406 QGQLGTLAFMAPEVLRCGOYGRSCDVWSVGCALIEMACAPPMNAEKSHNHLALIEKTA 1465
DB 561 RPSLOGSVFWMAPENVKQYSYTRKADIWSLIGCLVYEMMGTHPF---PCTQLQALFKIG 617
QY 1466 SATTAPSIPIHSPGLRDVALRCLQLQDPRPSELKHP 1506
DB 618 GSKASPTITDNASSEAKQFLAQTFFIDHNKRPSADEMLSP 658

RESULT 14
ID 09NYK3 PRELIMINARY; PRT; 619 AA.
AC 09NYK3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein kinase MEKK2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C., Lo H.;
RT "Cloning of human MEKK2 cDNA."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF239798; AAF63496.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR01245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; kinase; Transferase.
SQ SEQUENCE 619 AA; 69766 MW; 242B0F562D797873 CRC64;

Query Match 6.9%; Score 539.5; DB 4; Length 619;
Best Local Similarity 29.3%; Pred. No. 4.4e-25;
Matches 178; Conservative 78; Mismatches 205; Indels 147; Gaps 22;

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QY 1016 SASPOTR-----KFS-----LOFHNCPENKSDKLSPTVQSRPLPSSNIHRPKSR 1064
DB 35 SSSPKONDVAVFENRGEKRIILOFPVKLEDRSAKAKIAFGOSMDLHTYTNELVLP- 92
QY 1065 PTPGNTSKODPSKNSMTLDLNSSKCDSDSPGSSNSNAV-----IPS-----DETVETPV 1116
DB 93 -----LTTODDLKALELDRSITMKSLKILLVINGSTQATNLEPLRSLLEDLDVTFV-GA 146
QY 1117 ESKCRDLY-----NTELNS-----STEDILE----- 1137
DB 147 ERKRLSLIIGPTSRNDRSSPPPGYIPDELAHOVARNGSFTSINSEGEFIPESMEQMLDPLSL 206
QY 1138 -----ASMPSDDTYTFKSEVAVALSPKAEKNDYKXDVNNQCKEKM----- 1181
DB 207 SSPBNSGSGCPSLDSPLDSESTYPSKRMRAQSTPDNHQFSDNDPILFEFGKGYTPR 266
QY 1182 -----AAEERELALAIAMASASODALPIYQLOLVENGEDITITIQOD 1222
DB 267 RHYVYHHOEYNDGRKTFPPARRTQGNOLSPVSFS-----PTDHSITSSGSSIF----- 317
QY 1223 TPE-----TLPGHTKAKOPYREDTEWLKGOQIGLGAFFSSCYQADVG 1264
DB 318 TPEYDSDRIRRRSGSDIDNPTLTWMDISPPSRPAPTNMRLGKLLGGAGRGVLYCYDVD 377
QY 1265 TGTLMAYKQTYVRNTSSDEBEVYEAAREEIRMAHSHLNHNIITMLGATC-----EKSNNY 1320
DB 378 TGRBLAKVOYFDPD-SPETSKEVNALECEILOLKNLHERIYOYVG--CLRDPOEKTLS 434
QY 1321 LFTEMMAGSGVAHLISKYGAFFKESVINTTEQLRGLSYLHENQIHRDVGANLLDST 1380
DB 435 IFMEHYMGSSIKQOLKAYGLATEVNTYKRYTQILEGHVYHLSMAYVRDILKGANITLDST 494
QY 1381 GORLRIADFGAARLAS--KGTGAGEFQOGLGTTAFMAPEVLRGOYGRSCDQVMSVC 1437
DB 495 G-NKILGDFGASRKRLQITCLSGTG---MKSVGTGTPYKMSPEVTSGGGYGKADIMSVAC 549
QY 1438 AITEMACAPPMNAEKSHNLALIFKIASATFAPSTSHLSPGLRDVALKCLEQPODRP 1497
DB 550 TVEMETLEKPPW-AEFEA--MAALFKLATOPTNPKLPVHVSIDYTRDP-LKRIFEAKLRP 605
QY 1498 PSRELLKH 1505
DB 606 SADELRLH 613
RESULT 15
O9CAD5 PRELIMINARY: PRT: 883 AA.
AC O9CAD5:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 95.9 kDa protein.
GN F24D7.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehlerr E., Chan A., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
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RA Mullischer J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shin P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
DR EMBL: AC011622; AGS24246.1; -.
DR HSSP: 000534; 1B18.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser-Thr_Pkinase.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: Pf00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk.pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_AAP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Hypothetical protein; Transferase.
SQ SEQUENCE 883 AA; 95934 MW; 6A3FB18068F4318E CRC64;
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Query Match 6.98; Score 538.5; DB 10; Length 883;
Best Local Similarity 26.38; Pred. No. 8.7e-25;
Matches 182; Conservative 105; Mismatches 243; Indels 163; Gaps 29;

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QY 919 KLASSED-----ISE-----KLASISVGSSTTTTTTTTQ----- 951
DB 26 KLGFASDEDRSSGRKRRRRDEIVSERGALSRLSPSSPSTVSRCSQFAEASPAVPL 85
QY 952 PKPWQTKGRPHSQCLNS-----PLSHSQMLPALSPSSSTVSPVGRATD----- 1000
DB 86 PRPIV-----RHVYSTSGMNGSGRPGIDANLAKSWLPLRPHAT-SIPONTAEDEFA 140
QY 1001 ---VSKRLQGFIP-----CRIPSAPQTKRKSQFHRNCPENKSDKLSPVF 1046
DB 141 TASVSSGSGVDIPSDLSPLASDCENGNTPVNISRDQSMHNS--KNSAMFMRVP 197
QY 1047 TQSRPLPSSNIHRP-----KPSRP-----TPGNTSKQG- 1074
DB 198 NKNRILSAPRRPLGTHVKNLQIPQBDVLCAPDLSLSSPSRSPMRSEFIPDQVSHGL 257
QY 1075 DPSKNSMTLDLNSSKCDSDSPGSSNSNAVIPSD--ETVFTPYEERCRDLYNTELNSI 1132
DB 258 LISKRPYDVLISLGSQC--SSPGSGYNSGNSISGDMATQLFWP-QSKC-----SPECSPVP 311
QY 1133 EDLLEASMPSSDITVTEKSEVAVALSP--KAENDTYKQDVNNQCKEKEMAEEREL 1189
DB 312 SPRWTSFGPSRIG--SGAVTPLHPRAGSGTSGPTRRLDDNQGHR----- 357
QY 1190 AIAAMASADALPIYQLOLVENGEDITITIQODIPETLPHTKA-----KQPRD-- 1240
DB 358 -----LPLRP-----LLISNTCPFS-PYSAATSPSVSPARAATV 394
QY 1241 ---TEMLKGOIGLGAFFSSCYQADVGTGLMAKOVATYVRNTSSDEBEVYEAAREEIR 1297
DB 395 SPGRMKKGRGLMGSGCHYTLGFSNSESCEKAKETVLSDDPKRSE-AQOLGQELSV 453
QY 1298 MSHLNHNITRMIGATCEKSNYLFETMMAGSVAHLISKYGAFFKESVINTTEQLRGL 1357
DB 454 LSLRLRHONIVQYSGSEVVDKLYILEYVSGSITKLLQEGYGGENAIRNYTQOILSGL 513
QY 1358 SYLHENQIHRDVGANLLDSTGQRIADFGAANAALSKGTGAGFGQOLGTTAFMA 1417
DB 514 AYLAAKNTVHRDILGANILVDPHG-RVKVADFGAKHITAO-SGPISEK-----GSPYMA 567
QY 1418 PEVLRGOQYR-SCDVSVGCALITEMACAPPMNAEKSHNLALIFKIASATPAPSIPSH 1476
DB 568 PEVIKNSNGSLAVDIMSGLCTVLEMAATYKPPMS---QYEGVAPAMFKIGNSKEPLDPDH 624
QY 1477 LSPGLRDVALKCLEQPODRPPSRELLKHVFR 1509
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Db 625 LSEEGKDFVRKCLQRRNPANRPTTAQLDHAIVR 657

Search completed: December 20, 2002, 16:24:39
Job time : 80 secs

Query Match	Best Local Similarity	Matches 4647	Conservative	Mismatches	Indels	Gaps
23-JUL-1999;	99.0%;	Score 4564, 6;	DB 22;	Length 4693;		
23-JUL-1999;	99.0%;	Pred. No. 0;				
(ISIS-) ISIS PHARM INC.						
Monia BP, Cowser LM, Gaarde W, Ward DT;						
WPI: 2001-122264/13.						
P-PSDB: AAB60291.						
New antisense compound targeting nucleic acid encoding human						
mitogen-activated protein kinase kinase 1 (MEKK1), useful for treating						
diseases or conditions associated with MEKK1 expression, or preventing						
inflammation or tumor formation -						
Claim 1; Column 42-54; 35pp; English.						
This sequence represents human MEKK1 cDNA. MEKK1 (also known as mitogen-						
activated protein kinase kinase kinase 1, MEK kinase 1 and MAP/ERK						
kinase kinase 1) is a dual-specific serine/threonine kinase which						
mediates cellular responses to mitogenic stimuli, being involved in						
JNK/SAPK (Jun N-terminal kinase/stress-activated protein kinase) MAP						
kinase cascades. MEKK1 regulates signalling events associated with						
apoptosis (programmed cell death) and NF-kappa-B, both of which have						
been associated with the development of hyperproliferative disorders						
such as cancer. Specifically, MEKK1 lies directly downstream of Bcl-2						
in an apoptotic signalling cascade, and plays a critical role in the						
control of NF-kappa-B-mediated transcription at multiple points in the						
apoptotic cascade. The invention relates to antisense oligonucleotides						
targeted to the human MEKK1 gene, which inhibit its expression. A series						
of oligonucleotides (AA27086-AA27125) were designed to target different						
regions of the human MEKK1 RNA, and were analysed for their effect on						
MEKK1 mRNA levels by quantitative real-time PCR. The oligonucleotides of						
the invention are useful for diagnosis, prevention and treatment of						
conditions associated with MEKK1 expression, such as inflammation, and						
cancer and other hyperproliferative disorders.						
Sequence 4693 BP; 1340 A; 1102 C; 1143 G; 1108 T; 0 other:						
Query Match	87.0%;	Score 4564, 6;	DB 22;	Length 4693;		
Best Local Similarity	99.0%;	Pred. No. 0;				
Matches 4647; Conservative	0;	Mismatches	39;	Indels	9;	Gaps
65 CGAGCCCTGAGCAGGCGGCGGAGAGACCTCAAGCCGAGACGCGCCGCGGCTG	124					
2 CGAGCCCTGAGCAGGCGGCGGAGAGACCTCAAGCCGAGACGCGCCGCGGCTG	61					
125 CGCGGGAGACTGCTGGGGGAGGCGGAGCGGGGCGCCGAGCGGGGAGCTGGCGGCG	184					
62 CGCGGGAGACTGCTGGGGGAGGCGGAGCGGGGCGCCGAGCGGGGAGCTGGCGGCG	121					
185 GGCACCTGCGCAAGTGCAGTGTGGAGCTGGACACAGCTGCCTGAGCAGCGCTTTC	244					
122 GGCACCTGCGCAAGTGCAGTGTGGAGCTGGACACAGCTGCCTGAGCAGCGCTTTC	181					
245 TTGCGCGCTCACCGCGGCTCTCTGACTTCCCGTCCGCGGAGCCGCGAGCAGCGG	304					
182 TTGCGCGCTCACCGCGGCTCTCTGACTTCCCGTCCGCGGAGCCGCGAGCAGCGG	241					
305 GGAAGTGGAGCAGCGCTTCCAGCCTGTGGCGGCTGCGCGCCGACGAGGCGGAGCGG	364					
242 GGAAGTGGAGCAGCGGCTTCCAGCCTGTGGCGGCTGCGCGCCGACGAGGCGGAG	301					
365 GCGGCGCCACCTTACCGAGTGTGGCGGCGCGGACGAGCGCGCTTCCAGTCCCGAG	424					
302 GCGGCGCCACCTTACCGAGTGTGGCGGCGCGGACGAGCGCGCTTCCAGTCCCGAG	361					
425 GCGGCGAGCCCGGAGAAAGCGGCGCGCGCGGAGCGCTTCCAGTCCCGCGG	484					
362 GCGGCGAGCCCGGAGAAAGCGGCGCGCGCGGAGCGCTTCCAGTCCCGCGG	421					
485 CCGGCTGTGAGTGTGAGAAATTAAGAAATCTTAAAGCGTTTGGACAAGATGATGATC	544					
422 CCGGCTGTGAGTGTGAGAAATTAAGAAATCTTAAAGCGTTTGGACAAGATGATGATC	481					

QY	545	CAGAGAAACGAATGATCAGGGAGAAACTGAAAGCAACCTGTATGCGAGCGCTGGAAAGCAG	604
DB	482	CAGAGAAACGAATGATCAGGGAGAAACTGAAAGCAACCTGTATGCGAGCGCTGGAAAGCAG	541
QY	605	AATGGTTGGAAAGGAGAAATAGCGAGGCGCTGGTGTGTAATAACCAATCCAGATTAAAG	664
DB	542	AATGGTTGGAAAGGAGAAATAGCGAGGCGCTGGTGTGTAATAACCAATCCAGATTAAAG	601
QY	665	GAGATGATCTTGAAATGAAATCACTTACAGCTGAGTCTCCAGAGAGGTTCCAGGCAAGTG	724
DB	602	GAGATGATCTTGAAATGAAATCACTTACAGCTGAGTCTCCAGAGAGGTTCCAGGCAAGTG	661
QY	725	CGGCTTCACAGGCTTCCAAAGGGCGAGGAGTCCCTCTCTCTGGCAACTCCCATCAGGTC	784
DB	662	CGGCTTCACAGGCTTCCAAAGGGCGAGGAGTCCCTCTCTCTGGCAACTCCCATCAGGTC	721
QY	785	GCACAGTAAATTCAGAAATCTTCACAGAGTAAGAGAGAAAAAGATGTTCCCGAGTCCATTTC	844
DB	722	GCACAGTAAATTCAGAAATCTTCACAGAGTAAGAGAGAAAAAGATGTTCCCGAGTCCATTTC	781
QY	845	AGAGTGGCAATCAACACACACCCCGAAGAGCCCTTCACCAGATGCTTCACCATATA	904
DB	782	AGAGTGGCAATCAACACACACCCCGAAGAGCCCTTCACCAGATGCTTCACCATATA	841
QY	905	GCCCTGAGAGAAACAACCGCGGTGTTAAACAAAGTAAAGTGGGGGCAACGTACTTACGTC	964
DB	842	GCCCTGAGAGAAACAACCGCGGTGTTAAACAAAGTAAAGTGGGGGCAACGTACTTACGTC	901
QY	965	AGCAGATAGGGCCTTACTCTTCTCTGATTTGGAGAGACACGCCAGCAATTAATACCGGG	1024
DB	902	AGCAGATAGGGCCTTACTCTTCTCTGATTTGGAGAGACACGCCAGCAATTAATACCGGG	961
QY	1025	TGTTATTGGGCGCTCAGAACTGCAAGCTGTGCAGCTGGAAACATTCTGTATTCTTGTAT	1088
DB	962	TGTTATTGGGCGCTCAGAACTGCAAGCTGTGCAGCTGGAAACATTCTGTATTCTTGTAT	1022
QY	1085	TTGTGATCTCCGGGTGTTTCACTTAACCTTCAGACCCCAATGTAATGAGAGAAAACTT	1144
DB	1022	TTGTGATCTCCGGGTGTTTCACTTAACCTTCAGACCCCAATGTAATGAGAGAAAACTT	1088
QY	1145	TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACTAGAGCGCTAGCTCAAGGA	1204
DB	1082	TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACTAGAGCGCTAGCTCAAGGA	1144
QY	1205	TCAAGGCTCCATCTCTTATACACCATCCAGAAATTTGTTTCAGCAATGTCAATTTCTCAT	1266
DB	1142	TCAAGGCTCCATCTCTTATACACCATCCAGAAATTTGTTTCAGCAATGTCAATTTCTCAT	1201
QY	1266	CATTTCATCATAGTACTTCTACGCTAGTTCAGAAAAACACATPAAGATGGAAGAG	1324
DB	1202	CATTTCATCATAGTACTTCTACGCTAGTTCAGAAAAACACATPAAGATGGAAGAG	1266
QY	1325	AACAGATGTCTTATTTGCTTGTGGGCAATGCTTATGATGAAGAAAGCTTTACAGTGTG	1388
DB	1262	AACAGATGTCTTATTTGCTTGTGGGCAATGCTTATGATGAAGAAAGCTTTACAGTGTG	1321
QY	1385	AAGAGCGTGCAGGAACAAGTGCACACACACATCGCAATTTGGGCGAGAAAGTGTGA	1444
DB	1322	AAGAGCGTGCAGGAACAAGTGCACACACACATCGCAATTTGGGCGAGAAAGTGTGA	1381
QY	1445	GAAAGAAATAGAAACCTTTAATATGTCCTTGTATGATCTAAGTGGAGATCTCATGAT	1504
DB	1382	GAAAGAAATAGAAACCTTTAATATGTCCTTGTATGATCTAAGTGGAGATCTCATGAT	1441
QY	1505	TCATACGCGACAGTGTCAAGTCTGTGGATTCGCCCTTCTTCCTCAGAGCTGCACAGC	1564
DB	1442	TCATACGCGCGAGTGTCAAGTCTGTGGATTCGCCCTTCTTCCTCAGAGCTGCACAGC	1501
QY	1565	AGCAAAACGCTACACACAGCGCTTTGGCTGTGATCAAGAAAGATCAAGAGACCAATTTTA	1624
DB	1502	AGCAAAACGCTACACACAGCGCTTTGGCTGTGATCAAGAAAGATCAAGAGACCAATTTTA	1561

QY	1635	ACCTTACTCATTTAGGAAGCTCAGCAAAATCCCTTCGCTTACAAAGATTTTACGTAGCCAT	1684
Db	1562	ACCTTACTCATTTTGTGGAAGCTCAGCAAAATCCCTTCGCTTACAAAGATTTTACGTAGCCAT	1621
QY	1685	GGATTGAGGTTTGGAAATGGAATCGTGGCGCTTATTTTCTGAAACTGGAAATGGA	1744
Db	1622	GGATTGAGGTTTGGAAATGGAATCGTGGCGCTTATTTTCTGAAACTGGAAATGGA	1681
QY	1745	GAGAGATAGGCCCTCAGAGCGCTTTCCTCATGATGTCAGTGGGCGCCGTGTTGGCAATG	1804
Db	1682	GAGAGATAGGCCCTCAGAGCGCTTTCCTCATGATGTCAGTGGGCGCCGTGTTGGCAATG	1741
QY	1805	GGGAGAGCACTGGAAATTTCTGGGGGCGAGCAGTGGAAAGCAGCCGAGTGGGGGAGCCACA	1864
Db	1742	GGGAGAGCACTGGAAATTTCTGGGGGCGAGCAGTGGAAAGCAGCCGAGTGGGGGAGCCACA	1801
QY	1865	GTGGGTTCTTCCAGACCAGTATCTCAGGAGATGTGGTGGAGGCATGCTGCAAGCTTCGT	1924
Db	1802	GTGGGTTCTTCCAGACCAGTATCTCAGGAGATGTGGTGGAGGCATGCTGCAAGCTTCGT	1861
QY	1925	CAATGCTCTGTGCGACCCGTCTACAAAAGTGAATCTGCTCTTTAAAAACATTGAGAG	1984
Db	1862	CAATGCTCTGTGCGACCCGTCTACAAAAGTGAATCTGCTCTTTAAAAACATTGAGAG	1921
QY	1985	CCATGCTGTATATACTCTTGTGCGACAGTTTAAACGGAAGATCAAACTTCAGAGACTTC	2044
Db	1922	CCATGCTGTATATACTCTTGTGCGACAGTTTAAACGGAAGATCAAACTTCAGAGACTTC	1981
QY	2045	TCCAGGCCAGTTGTAGACACCATCTTGTGTAATGTGCAGATGCCAATAGCCGACAGTC	2104
Db	1982	TCCAGGCCAGTTGTAGACACCATCTTGTGTAATGTGCAGATGCCAATAGCCGACAGTC	2041
QY	2105	AGCTGTCATATCAACACCTTGTGGAACCTGCAAAAGCCAGACAGAGAGTTGGCAGTGTG	2164
Db	2042	AGCTGTCATATCAACACCTTGTGGAACCTGCAAAAGCCAGACAGAGAGTTGGCAGTGTG	2101
QY	2165	GCAGAGAAATCTPAAAAGCTGATGCCATTGTATTTGGTGGTGGTATATGTCTTAAAT	2224
Db	2102	GCAGAGAAATCTPAAAAGCTGATGCCATTGTATTTGGTGGTGGTATATGTCTTAAAT	2161
QY	2225	GATATCTTGGAAACCAACAGTATCAAAACAAATTTGGCAAAATTTTGGCGGCTTGTTC	2284
Db	2162	GATATCTTGGAAACCAACAGTATCAAAACAAATTTGGCAAAATTTTGGCGGCTTGTTC	2221
QY	2285	TTATAGATAGACTGTTTGTGGAATTTCTGCTGATATTTATCTCATATTTGTCACTACTG	2344
Db	2222	TTATAGATAGACTGTTTGTGGAATTTCTGCTGATATTTATCTCATATTTGTCACTACTG	2281
QY	2345	ATGTTTCACAAGCTGACCTGTTTGAATCAGGATATAGAAAGCTGCTGTCCTTAACT	2404
Db	2282	ATGTTTCACAAGCTGACCTGTTTGAATCAGGATATAGAAAGCTGCTGTCCTTAACT	2341
QY	2405	TTGCTTTGCAGTCCATTGATTAATTTCCCACTCAATGTTGGCAAACTTTCAGAGAGATCT	2464
Db	2342	TTGCTTTGCAGTCCATTGATTAATTTCCCACTCAATGTTGGCAAACTTTCAGAGAGATCT	2401
QY	2465	ACTTGAGTCTGCAAGAATGTTGTTACTACAGATACCCATGTTTTCAAAACGTTAGAAA	2524
Db	2402	ACTTGAGTCTGCAAGAATGTTGTTACTACAGATACCCATGTTTTCAAAACGTTAGAAA	2461
QY	2525	TGCTGAGTGTTCAG--TTCCACTCACTTCAACAGATGCGTGCCGTTTGATGAGCTA	2581
Db	2462	TGCTGAGTGTTCAGTGTTCCTCACACACATTCACAGATGCGTGCGGTTTGATGAGCTT	2521
QY	2582	TTGCAAGATGAGTGGAAATTTGCCGAAGCACTCCAGTTGGGGCTAGAAAGACTTTTGATG	2641
Db	2522	ATGCAAGATGAGTGGAAATTTGCCGAAGCACTCCAGTTGGGGCTAGAAAGCACTTTTAAAC	2581
QY	2642	GTCACACAGAGAGC--TTCTTGCAGGAGATGTTTCCCAACAATCTATGAGAAACACAGA	2699
Db	2582	GACACACACACACAGCTTTTGCAGAGCATGTGTTCCCAACAATCTATGAGAAACACAGA	2641
QY	2700	GAAACAGTTTCCC--TGAGTGCACAGTCCATTTACAGAAACTGGAAAAGGATATATGTCTA	2758

Db	2642	GAACAGTCCCTTGAGTGCACAGTCCATTGTAGACAAAACCTGGAAAAAGATTAATGTCTGA	2701
QY	2759	CAAAATGAGTGGCAGTTCAGAGACATTTTCGAGAGATGTGGCCAGCATTTTCATGATGAGAC	2818
Db	2702	CAAAATTCAGTGGCCAGTTTCAGAGACAAATTTCTGAGAGATGGCCAGGATTTTCAGTAGAGAC	2761
QY	2819	CTTCTAGTTCAAACAAACAAACAAACAAACAAACAAACAGACAAACCAAGCAATGGTTCAAA	2878
Db	2762	CTTCTAGTTCAAACAAACAAACAAACAAACAAACAAACAGACAAACCAAGCAATGGTTCAAA	2821
QY	2879	CAAAAAGCAGACCCACAGTCACTGTGTTGAACTCTCTCTTATCTCATCATTTCCCAAT	2938
Db	2832	CAAAAAGCAGACCCACAGTCACTGTGTTGAACTCTCTCTTATCTCATCATTTCCCAAT	2881
QY	2939	TAAATGTTCCAGCCTTTCTCAACCCCTTTCTTCTTACCCCATCTGTACCAGCTGGCACTG	2998
Db	2882	TAAATGTTCCAGCCTTTCTCAACCCCTTTCTTCTTACCCCATCTGTACCAGCTGGCACTG	2941
QY	2999	CAACAGATGTCTCTTAACCATAGACTTCACAGGATTCATTCCTCGCAGAAATACCTTCAT	3058
Db	2942	CAACAGATGTCTCTTAACCATAGACTTCACAGGATTCATTCCTCGCAGAAATACCTTCAT	3001
QY	3059	CTCCTCAAAACACAGCCGCAAGTTTTCTCTCAATTCACAGAAACTGTCTCTGAAAAACAAG	3118
Db	3002	CTCCTCAAAACACAGCCGCAAGTTTTCTCTCAATTCACAGAAACTGTCTCTGAAAAACAAG	3061
QY	3119	ACTCAGATTAACCTTCCCCAGCTCTTACTACGTCAAGACCCCTGCCCTCCAGTAACATAC	3178
Db	3062	ACTCAGATTAACCTTCCCCAGCTCTTACTACGTCAAGACCCCTGCCCTCCAGTAACATAC	3121
QY	3179	ACAGGCCAAAGCCCATCTAGACCTTACCCCAAGGTAATCAAGTAACAGGAGAGATCCCTCAA	3238
Db	3122	ACAGGCCAAAGCCCATCTCTGACACTTACCCCAAGTATACAAAGTAACAGGAGAGATCCCTCAA	3181
QY	3239	AAAAATAGCATACACTTGATCTGAAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTA	3298
Db	3182	AAAAATAGCATACACTTGATCTGAAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTA	3241
QY	3299	GCACCATAGTAAGTAATGCGTGTATATCCACAGTGCAGACACATGTTCACCCCAAGTAGAGG	3358
Db	3242	GCACCATAGTAAGTAATGCGTGTATATATCCACAGTGCAGACACATGTTCACCCCAAGTAGAGG	3301
QY	3359	AGAAATGCAGATTTAGATGTCAATACAGAGTCACATCCAGTATTTGAGAGCCCTCTTGAG	3418
Db	3302	AGAAATGCAGATTTAGATGTCAATACAGAGTCACATCCAGTATTTGAGAGCCCTCTTGAG	3361
QY	3419	CATCTATGCCCTTCAAGTATACAAACAGTAACCTTTAAGTCAGAAAGTTGCTGTCTGTCTC	3478
Db	3362	CATCTATGCCCTTCAAGTATACAAACAGTAACCTTTAAGTCAGAAAGTTGCTGTCTGTCTC	3421
QY	3479	CTGAAAAAGCGTGAATAATGATGATACCTACCAAGATATGTGATATATATCAAAAGTGTCA	3538
Db	3422	CTGAAAAAGCGTGAATAATGATGATACCTACCAAGATATGTGATATATCAAAAGTGTCA	3481
QY	3539	AAGAGAGATGATGAAGCTGGAAGAAGAAGACCTTTACCATTTCCATGGCAATGTCAAGCT	3598
Db	3482	AAGAGAGATGATGAAGCTGGAAGAAGAAGACCTTTACCATTTCCATGGCAATGTCAAGCT	3541
QY	3599	CTCAGATGCCCTTCCCATAGTTCTCAGCTGCAGGTTGAAAAATGGAGAAGATATCATCA	3658
Db	3542	CTCAGATGCCCTTCCCATAGTTCTCAGCTGCAGGTTGAAAAATGGAGAAGATATCATCA	3601
QY	3659	TTATTTCAACAGGATATCACACAGACATCTTACACAGACATACCAAACCAACACCGTATA	3718
Db	3602	TTATTTCAACAGGATATCACACAGACATCTTACACAGACATACCAAACCAACACCGTATA	3661
QY	3719	GAGAGAGACATGATGTGCTCAAAAGTCTCAACAGATAGCCCTTGAGAGATTTCTCTTGATT	3778
Db	3662	GAGAGAGACATGATGTGCTCAAAAGTCTCAACAGATAGCCCTTGAGAGATTTCTCTTGATT	3721
QY	3779	ATCAGGCTCAAGATGTGGGAAGTGAACCTTAATGCGCTGTTAAACAGGTGACTTAATGTCA	3838

Db	3732	ATCAGGCTCAAGATGTGGAACTGGAACTTTAAATGGCTCTTAAACAGGTGACTTAATGTCA	3781
Qy	3839	GAACACACTCTTTCGACCAAGAAGTAGTAGAACCACTAAGAGAGAGATAAAGATGA	3898
Db	3782	GAACACACTCTTTCGACCAAGAAGTAGTAGAACCACTAAGAGAGAGATAAAGATGA	3841
Qy	3899	TGAGCCATCTGAAATCATCCAAACATCATTTTNGATGTTGGGAGCCAGTGTGGAAGACGA	3958
Db	3842	TGAGCCATCTGAAATCATCCAAACATCATTTAGATGTTGGGAGCCAGTGTGGAAGACGA	3901
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Db	3902	ATTACAACTCTTATATGAATGGATGGGAGATCGGTGGCTCATTTTGGTAGTAAT	3961
Qy	4019	ATGGAGCCCTTCAAAAGATTCAGTAGTTATTAACTACACTGAAAGTTACTCCGTGGCTTT	4078
Db	3962	ATGGAGCCCTTCAAAAGATTCAGTAGTTATTAACTACACTGAAAGTTACTCCGTGGCTTT	4021
Qy	4079	CGTATCTCCATGAAACCAATCATTCACAGAGATGTCAAAGTGGCAATTTGCTAATTG	4138
Db	4022	CGTATCTCCATGAAACCAATCATTCACAGAGATGTCAAAGTGGCAATTTGCTAATTG	4081
Qy	4139	ACAGACTGGTCAGACAGACTAAGAAATGGAGATTTTGGACTGCAGCGAGTGGCATAA	4198
Db	4082	ACAGACTGGTCAGACAGACTAAGAAATGGAGATTTTGGACTGCAGCGAGTGGCATAA	4141
Qy	4199	AAGGAAGTGTGTCAGAGAGATTTCAAGGACATTTACTGGGGCAATTCATTAATATGCGAC	4258
Db	4142	AAGGAAGTGTGTCAGAGAGATTTCAAGGACATTTACTGGGGCAATTCATTAATATGCGAC	4201
Qy	4259	CTGAGGTACTAAGAGGTCAACAGATNAGGAAGAGCTGATATNAGATGTGGCTGTG	4318
Db	4202	CTGAGGTACTAAGAGGTCAACAGATNAGGAAGAGCTGATATNAGATGTGGCTGTG	4261
Qy	4319	CTAATTAAGAAATGGCTTGTGCAAAACCAACATGGAATCAGAAAAACACTCCATCATC	4378
Db	4262	CTAATTAAGAAATGGCTTGTGCAAAACCAACATGGAATCAGAAAAACACTCCATCATC	4321
Qy	4379	TTTGCTTGCATATTTAAGATTTGCTAATGCAACTACGTCTCCATGCATCCCTTCACATTTGT	4438
Db	4332	TTTGCTTGCATATTTAAGATTTGCTAATGCAACTACGTCTCCATGCATCCCTTCACATTTGT	4381
Qy	4439	CTCCGGTTTACGAGATGTGGGCTTCGTGTTTGAATCTCAACTCAGACAGACCTC	4498
Db	4382	CTCCGGTTTACGAGATGTGGGCTTCGTGTTTGAATCTCAACTCAGACAGACCTC	4441
Qy	4499	CATCAAGAGAGACTACTGAAACATCCAGTCTTTTCGTACTCATGTATAGCAATTAATGAGA	4558
Db	4442	CATCAAGAGAGACTACTGAAACATCCAGTCTTTTCGTACTCATGTATAGCAATTAATGAGA	4501
Qy	4559	TCAAACTACAGTACGAACAGATGCTCAACAGAGAAAAAACTTGTGGGGAACCACTT	4618
Db	4502	TCAAACTAC - GTAGAAACAGATGCTCAACAGAGAAAAAACTTGTGGGGAACCACTT	4560
Qy	4619	GATATTTTACAGGGCATGATGSCCATCGAAGACAGTATGAACGAGGCGAGGGGAAACCTT	4678
Db	4561	GATAT - - CTACGGCCATGATGCCACTGACAGCTATGAACGAGGCGAGGGGAAACCTT	4618
Qy	4679	ACCTAAGTATGTGATGACAAATCATGATCTGTACCTAAAGTCAGTATGCAAAAGCCAA	4738
Db	4619	ACCTAAGTATGTGATGACAAATCATGATCTGTACTTAAGTCAGTATGCAAAAGCCAA	4678
Qy	4739	ACTAGTCAGAAACT 4753	
Db	4679	ACTAGTCAGAAACT 4693	

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RESULT 2
AA168699
ID    AA168699 standard; DNA; 4693 BP
XX
AC    AA168699;
XX

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DT		21-JAN-2002	(first entry)
XX			
DE		Human MEK kinase MEK1 encoding DNA.	
XX			
KW	Oncogene; c-raf-1; human; MEK1; MEK kinase; raf-binding; cytosolic;		
KM	mitogen activated and extracellular stimuli regulated kinase;		
KW	gene therapy; NF-kB suppression; tumour cell proliferation;		
KM	NF-kB-mediated signal cascade; ds.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..4488	
FT		/tag= "a"	
FT		/product= "MEK1"	
FT		/partial	
FT		/note= "no start codon given"	
XX			
PN	WO200179501-A2.		
XX			
PD	25-OCT-2001.		
XX			
PF	17-APR-2001; 2001WO-DE01518.		
XX			
PR	14-APR-2000; 2000DE-1020138.		
XX			
PA	(RAPP/) RAPP U R.		
PA	(WIRTH/) WIRTH T.		
PI	Rapp UR, Wirth T;		
XX			
DR	WPI; 2002-017617/02.		
XX	P-PSDB; AAG80184.		
PT	New nucleic acid encoding partial raf sequence, useful for identifying		
PT	compounds that block binding of raf to its activating kinase as		
PT	potential anticancer agents		
XX			
PS	Disclosure: Fig 11b-d; 66pp; German.		
XX			
CC	This invention describes a novel nucleic acid (I) that: (i) encodes at		
CC	least one raf partial sequence containing a MEK1 (mitogen activated and		
CC	extracellular stimuli regulated (MEK) kinase) binding site; (ii) encodes		
CC	at least one partial sequence of MEK1 containing a raf binding site;		
CC	(iii) is a silent mutation of (i) or (ii); or (iv) hybridizes to		
CC	(i)-(iii). The products of the invention have cytostatic activity and can		
CC	be used for gene therapy. The products also suppress NF-kB activation		
CC	resulting in inhibition of tumour cell proliferation or transformation.		
CC	(i), or proteins/peptides encoded by them, are useful for identifying		
CC	compounds that block binding of raf to MEK1. These compounds, optionally		
CC	where expressed from gene therapy vectors, are useful in human or		
CC	veterinary medicine for treatment of tumors. Antisense sequences, or		
CC	ribozymes, that bind to (i) are used to inhibit MEK1 activation. Also		
CC	nucleic acid (I') encoding at least a part of raf (or its silent		
CC	mutations or hybridizing sequences) is used to examine interaction of		
CC	encoded proteins with activation of the NF-kB-mediated signal cascade and		
CC	to screen for inhibitors of cell transformation by raf-mediated		
CC	activation of NF-kB. This sequence encodes the human MEK1 protein		
CC	described in the method of the invention.		
XX			
SQ	Sequence 4693 BP; 1340 A; 1102 C; 1143 G; 1108 T; 0 other;		
	Query Match	87.0%; Score 4564.6; DB 24; Length 4693;	
	Best Local Similarity	99.0%; Pred. No. 0;	
	Matches 4647; Conservative	0; Mismatches 39; Indels 9; Gaps 5;	
OY	65 CGAGCCTTGAGGACGAGCGGCGGAGGAGGCCCTCAAGCGGAGCGCGCGGGGCTG	124	
DB	2 CGAGCCCTTGAGGACGAGCGGCGGCGGAGGAGGCCCTCAAGCGGAGCGCGCGGGGCTG	61	
OY	125 CCGCGGAGCATGCTGCAGGAGCGGCGGCGGCGGCGGCGGCGGAGCATGCGGCGGCGG	184	
DB	62 CCGCGGAGCATGCTGCAGGAGCGGCGGCGGCGGCGGCGGCGGAGCATGCGGCGGCGGCGG	121	

QY 185 GGCAGCTGGCAAAAGTGGCAGTGTGGAGCTGGACCAAGCTGCTGAGCAGCCGCTCTTC 244
DB 122 GGCAGCTGGCAAAAGTGGCAGTGTGGAGCTGGACCAAGCTGCTGAGCAGCCGCTCTTC 181
QY 245 TTGGCCGCTCAGCCGCGGCTCTCGACTTTCCCGCGTGGCGGAGCCCGCGGAGCAGCGG 304
DB 182 TTGGCCGCTCAGCCGCGGCTCTCGACTTTCCCGCGTGGCGGAGCCCGCGGAGCAGCGG 241
QY 305 GGAGTGGGAGCCGCTTCAGACCTGTGGCGGTGGCGCCGCGCCAGAGCCGCGAGCGCG 364
DB 242 GGAAGTGGAGACCGGCTTCAGACCTGTGGCGGTGGCGCCGCGCCAGAGCCGCGAGCGCG 301
QY 365 GCGGCGCCCACTTACCGAGTCGCTGGCGCGCGCGGAGCAGCGGCGCTCGAGTCCGCGAG 424
DB 302 GCGGCGCCCACTTACCGAGTCGCTGGCGCGCGCGGAGCAGCGGCGCTCGAGTCCGCGAG 361
QY 425 GCGGCGAGCCCGGAGAGCCGCGGCGCGCGCGCGAGCCGCTCTCGAGCAGCGGCGCGCG 484
DB 362 GCGGCGAGCCCGGAGAGCCGCGGCGCGCGCGCGAGCCGCTCTCGAGCAGCGGCGCGCG 421
QY 485 CGGCTGTGAGTGGAGAACTCTCAAGAGGTTGCACAAAGATGGATGCTC 544
DB 422 CGGCTGTGAGTGGAGAACTCTCAAGAGGTTGCACAAAGATGGATGCTC 481
QY 545 CAGAGAACGAATGATCAGGAGAGAACTGAGGCAACCTGTATGCCAGCGCTGGAAGCAG 604
DB 482 CAGAGAACGAATGATCAGGAGAGAACTGAGGCAACCTGTATGCCAGCGCTGGAAGCAG 541
QY 605 AATGGTTGAAAGGAAATATAGCGAGGCGCTGTGGTGGTAAACCAATCCCGATTAAAG 664
DB 542 AATGGTTGAAAGGAAATATAGCGAGGCGCTGTGGTGGTAAACCAATCCCGATTAAAG 601
QY 665 GAGATGATCTGAAATGAATCACTTAGCAGTGAAGTCTCCAGAGAGAGTCCAGGCAAGT 724
DB 602 GAGATGATCTGAAATGAATCACTTAGCAGTGAAGTCTCCAGAGAGAGTCCAGGCAAGT 661
QY 725 CGGCTTACCAAGCTTCCAAAGCCGAGCGAGTCTCTGCGCAACTCCCATCAGGTC 784
DB 662 CGGCTTACCAAGCTTCCAAAGCCGAGCGAGTCTCTGCGCAACTCCCATCAGGTC 721
QY 785 GCACATGAAATCAGATCTCCAGAGTGAAGGAGAAAGATTTCCCGATGCGCTTTC 844
DB 722 GCACATGAAATCAGATCTCCAGAGTGAAGGAGAAAGATTTCCCGATGCGCTTTC 781
QY 845 AGAGTGGCAGAAATCACACCAACCCGGAAGAGCCCTTACAGATGGCTTCTCAACATATA 904
DB 782 AGAGTGGCAGAAATCACACCAACCCGGAAGAGCCCTTACAGATGGCTTCTCAACATATA 841
QY 905 GCCCTGAGAAACAAACCCGCGGTGTTAACAAAGTATGCGGCGCAGACTGTACTTATGC 964
DB 842 GCCCTGAGAAACAAACCCGCGGTGTTAACAAAGTATGCGGCGCAGACTGTACTTATGC 901
QY 965 AGCAGATAGAGGCTTAATCTCTTCTGATTTGAGAGAGCAGCCGAGCAAAATATACCGG 1024
DB 902 AGCAGATAGAGGCTTAATCTCTTCTGATTTGAGAGAGCAGCCGAGCAAAATATACCGG 961
QY 1025 TGTATTATGGGCTTCAGAACTGAGCTGTGACGTGGAAATCTGTGATTCATCTGAT 1084
DB 962 TGTATTATGGGCTTCAGAACTGAGCTGTGACGTGGAAATCTGTGATTCATCTGAT 1021
QY 1085 TTGTGATGCTCGGCGGTGTTCAACTAGAACCTTACAGACCCAAATGTTATGAGAAAACTT 1144
DB 1022 TTGTGATGCTCGGCGGTGTTCAACTAGAACCTTACAGACCCAAATGTTATGAGAAAACTT 1081
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QY 1205 TCAAAAGCTCCATCTCGTAAACCAATCCAGAAAGTTGTTTCCAGCAATGCTCAAAATTCATATA 1264
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DB 1382 GAAGAAATTAAGAACTTTAATATGTCCTTGTGTAGATCTTAAGTGGAGATCTCATGAT 1441
QY 1505 TCTACAGCCAGAGTTGTCAGATTCAGTCCGCTGATTCCTCTCCAGAGCTGCACAGC 1564
DB 1442 TCTACAGCCAGAGTTGTCAGATTCAGTCCGCTGATTCCTCTCCAGAGCTGCACAGC 1501
QY 1565 AGCAAAACCTTACAGACAGCAGCTTTGGCTGGATCAGCAAGAAATCAAGAGAGCAATTTTA 1624
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QY 2525 TGCCTGAGTTTCCAG--TTCCACATCACTTCCACAGATGCGTGCGCTTGTGATGCTA 2581
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QY 2582 TTGAGATGAGGTGGAATTTGCCGAAGCCATCAGTTGGGCGTGAAGAACACTTTGGATG 2641
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QY 2642 GTTCAACAGGACAGC--TTCTTTGACAGCATCTGTTCCCAACAACTATCTGGAACACAGA 2699
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QY 2999 CAACAGATGCTCTTAAGCATATAGACTTTCAGAGATTCATTCCTCGCAGAAATACCTTCTGCAAT 3058
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Db 3722 ATCAGGCTCAAGTGTGGAGTGCAGAACTTTAATGGCTTTAAACAGTGCATTAATGCA 3781
QY 3839 GAAACACATCTTCTGAGCAAGAAAGATAGTAGAGCACTAAGAGAGATTAAGATGA 3898
Db 3782 GAAACACATCTTCTGAGCAAGAAAGATAGTAGAGCACTAAGAGAGATTAAGATGA 3841
QY 3899 TGAGCATCTGAATCATCCAAACATCATTTAGATGTTGGAGCCACGTGTGAAGAGCA 3958
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Db 3902 ATTACATCTCTTCAATGAATGATGGAGGAGATCGGTGGCTCATTTGCGAGATTAAT 3961
QY 4019 ATGAGCCCTTCAAGAAAGATAGTATTAATTAACACTAAGAGTACTCGTGCCCTTT 4078
Db 3962 ATGAGCCCTTCAAGAAAGATAGTATTAATTAACACTAAGAGTACTCGTGCCCTTT 4021
QY 4079 CGTATCTCCATGAAAACCAATCATTTACAGAGATGTCAAAGGTGCAATTTGCTAATTTG 4138
Db 4022 CGTATCTCCATGAAAACCAATCATTTACAGAGATGTCAAAGGTGCAATTTGCTAATTTG 4081
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Db 4262 CTATTATAGAAATGGCTTGTGCAAAACACAGTGAATGCAGAAAACCTCAATCAATC 4321
QY 4379 TTGCTTTGATATTTAAGATTTGCTAGTCAACTACTGCTCATCGATCCCTTCAATTTGT 4438
Db 4322 TTGCTTTGATATTTAAGATTTGCTAGTCAACTACTGCTCATCGATCCCTTCAATTTGT 4381
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QY 4499 CATCAAGAGAGTACTGAAGAGTCCAGTCTTGTGACTACAGTGTAGCCAAATTAAGCAGA 4558
Db 4442 CATCAAGAGAGTACTGAAGAGTCCAGTCTTGTGACTACAGTGTAGCCAAATTAAGCAGA 4501

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D 902 AGCAGATAGGGCCTACCTCTTCCCTGATTGGAGAGACACGCCAGACAATTAATACC6G 961
O 1025 TGTATTATGGGCTCAGAACTGACGTGTGCACGTGGAACTTCTGTATTCATCTGCTAT 1084
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D 1022 TTGTGATGCTCCGGGCTGTTCAACTGAACTTCAACCCCAATGTTATGAGAAAACTT 1081
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D 1142 TCAAAAGCTCATCTGCTAATCACCATCCAGAAAGTTGTTTCAGGATGCAATTTCTCAT 1201
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D 1202 CATGTGCATCATCTGCTAATCACCATCCAGAAAGTTGTTTCAGGATGCAATTTCTCAT 1261
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O 1505 TCTACAGCAGAGTTGTCAAGTCTGTGATTTCCCTTCTTCCCTCAGAGCTGCACAG 1564
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D 1622 GGATTCAGGTGTTGGAAATGGAATCGTGTGCTTATTTTCTAGAACTGGAATGTGA 1681
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D 1742 GGGAGAGCAGCTGGAATTTGGGGGAGCAGTGGAGAGCAGCCGAGTGGGGGAGCCACCA 1801
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O 1925 CAATGGTCTGTGCTGACCTGTCTACAAAGTGTAGCTGCTGCTTTAAACATTTGAGAG 1984
D 1862 CAATGGTCTGTGCTGACCTGTCTACAAAGTGTAGCTGCTGCTTTAAACATTTGAGAG 1921
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RESULT 4
 AAS6059
 ID AAS6059 standard; cDNA; 4492 BP.
 AC AAS6059;
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #1863.
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Dmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR P-PSDB; ABG01872.
 DR New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PS Claim 1; SEQ ID No 1863; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

Sequence 4492 BP: 1266 A; 1057 C; 1101 G; 1067 T; 1 other:

Query Match 83.0%; Score 4354; DB 23; Length 4492;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 4445; Conservative 0; Mismatches 36; Indels 10; Gaps 6;

QY 65 CGAGCCTGAGGAGCGCGCGGAGAGCCTCAAGCGAGAGCGCGCGCGCTG 124
DB 2 CGAGCCTGAGGAGCGCGCGGAGAGCCTCAAGCGAGAGCGCGCGCGCTG 61
QY 125 CGCGGAGACTGCTGGGAGGCGGAGCGGCGGCGGAGCGGCGGAGCTGGCGCGG 184
DB 62 CGCGGAGACTGCTGGGAGGCGGAGCGGCGGCGGAGCGGCGGAGCTGGCGCGG 121
QY 185 GCGAGCTGCGCAAGTGCAGAGTGTGAGCTGAGCAGCTGCTGAGCAGCGCTCTTC 244
DB 122 GCGAGCTGCGCAAGTGCAGAGTGTGAGCTGAGCAGCTGCTGAGCAGCGCTCTTC 181
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DB 182 TTGCGCCTCAGCGCGCGCTCTCTCACTTCCCGTGCAGCGCGCGGAGCGAGCGG 241
QY 305 GAGTGGAGCGGCTTCAGAGCTGTGGCGGTGCGCGCGCGCGAGCGGAGCGGAGCGG 364
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QY 425 CGCGCGAGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCTGAGTCCGAGCGGCGG 484
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DB 422 CGCGTGTGAGATGGAATTAAGAACTCTCAAGGTTGCAAGATGATGATGCTG 481
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QY 3299 GCAGCAATAGTAAATGCTGTATACCCAGTGAAGACAGTGTGTCACCCCAAGAGG 3358
Db 3242 GCAGCAATAGTAAATGCTGTATACCCAGTGAAGACAGTGTGTCACCCCAAGAGG 3301
QY 3359 AGAAATGAGATTAATGATCTCAATACAGAGCTCAACTCCAGTATTTAGAGACCTGTTGA 3418
Db 3302 AGAAATGAGATTAATGATCTCAATACAGAGCTCAACTCCAGTATTTAGAGACCTGTTGA 3361
QY 3419 CATCTATGCTTCAAGTATACACAGTAACTTTTAAGTGAAGTGTCTGCTGCTC 3478
Db 3362 CATCTATGCTTCAAGTATACACAGTAACTTTTAAGTGAAGTGTCTGCTGCTC 3421
QY 3479 CTGAAAAGGCTGAAAATGATGATACCTTCAAAAGATGATGTAATCATTAATGAAAAGTGA 3538
Db 3422 CTGAAAAGGCTGAAAATGATGATACCTTCAAAAGATGATGTAATCATTAATGAAAAGTGA 3481
QY 3539 AAGAGAGATGGAAGCTGGAAGAAGAGCTTTAGCAATTTGCCATGGAATGTCAGCGT 3598
Db 3482 AAGAGAGATGGAAGCTGGAAGAAGAGCTTTAGCAATTTGCCATGGAATGTCAGCGT 3541
QY 3599 CTCAGATGCTTCCCATATGTTCTCAGCTGCAAGTTGAAAATGGAAGATATCATCA 3658
Db 3542 CTCAGATGCTTCCCATATGTTCTCAGCTGCAAGTTGAAAATGGAAGATATCATCA 3601
QY 3659 TTATTTCAACAGATATACACAGACTTACAGAGCAATACCAAGCAAAACCAACCGTATA 3718
Db 3602 TTATTTCAACAGATATACACAGACTTACAGAGCAATACCAAGCAAAACCAACCGTATA 3661
QY 3719 GAGAAGACATGAAATGCTGGAAGGTCACAAGATAGCCCTTGGAGCATTTCTCTGTT 3778
Db 3662 GAGAAGACATGAAATGCTGGAAGGTCACAAGATAGCCCTTGGAGCATTTCTCTGTT 3721
QY 3779 ATCAGGCTCAAGATGTGGAACTGGAATTTAATGGCTTTAAACAGTGTACTATGCA 3838
Db 3722 ATCAGGCTCAAGATGTGGAACTGGAATTTAATGGCTTTAAACAGTGTACTATGCA 3781
QY 3839 GAAACACATCTTCTGAGCAAGAAGAGTGAAGCACTTAAGAAAGAGATTAAGAAATGA 3898
Db 3782 GAAACACATCTTCTGAGCAAGAAGAGTGAAGCACTTAAGAAAGAGATTAAGAAATGA 3841
QY 3899 TGAGCCATCTGAATCATCAAAACATCATTAAGATGTTGGAGCCACGTTGTAGAAGACA 3958
Db 3842 TGAGCCATCTGAATCATCAAAACATCATTAAGATGTTGGAGCCACGTTGTAGAAGACA 3901
QY 3959 ATTCAATCTCTTCAATTAATGATGGAAGGGGATTCGGTGCATTTGCTGATTAAT 4018
Db 3902 ATTCAATCTCTTCAATTAATGATGGAAGGGGATTCGGTGCATTTGCTGATTAAT 3961
QY 4019 ATGAGCCTTCAAAAGAAATCAGTAAATTAATACATACGAACAGTACTTCCGTGCCCTT 4078
Db 3962 ATGAGCCTTCAAAAGAAATCAGTAAATTAATACATACGAACAGTACTTCCGTGCCCTT 4021
QY 4079 CGTATCTCCATGAAAACCAAAATCATATTCACAGAGATGTCAAAAGTGCATTAATTTG 4138
Db 4022 CGTATCTCCATGAAAACCAAAATCATATTCACAGAGATGTCAAAAGTGCATTAATTTG 4081
QY 4139 ACAGACTGTGTACAGAGATTAAGATTTTGGAGCTGCAAGCTGAGTTGGCATCA 4198
Db 4082 ACAGACTGTGTACAGAGATTAAGATTTTGGAGCTGCAAGCTGAGTTGGCATCA 4141
QY 4199 AAGCAATGTGTGAGAGAGTTTTCAGAGACAATTACTGGGGAACAATTCATTTATGGAC 4258
Db 4142 AAGCAATGTGTGAGAGAGTTTTCAGAGACAATTACTGGGGAACAATTCATTTATGGAC 4201
```


QY 4259 CTGAGCTACTAAGAGCTCAACACTATGGAAGAGCTGTGTATGTAGTGTGGCTGTG 4318
 DB 4202 CTGAGCTACTAAGAGCTCAACACTATGGAAGAGCTGTGTATGTAGTGTGGCTGTG 4261
 QY 4319 CTAATTATGAATGGCTGTGCAAAACCAACGAAATGAGAAAACACTCCAAATCAGC 4378
 DB 4262 CTAATTATGAATGGCTGTGCAAAACCAACGAAATGAGAAAACACTCCAAATCAGC 4321
 QY 4379 TTGCTTTGATTTTAAATGCTAGTGAACACTACTGCTCATGATCCCTTCAATTTGT 4438
 DB 4322 TTGCTTTGATTTTAAATGCTAGTGAACACTACTGCTCATGATCCCTTCAATTTGT 4381
 QY 4439 CTCTGCTGTTTACG-AGATGTGGCTCTTGTGTTT-AGAACTTCAACT--CAGAACAGA 4494
 DB 4382 CTCTGCTGTTTACGAGATGTGGCTCTTGTGTTTAAAGAACTTCAACTTCAAGACAGA 4441
 QY 4495 CCMCCATCAAGAGAGCTACTGAAGCATCCAGTCTTGTGACTTCAATGATG 4545
 DB 4442 CCMCCATCAAGAGAGCTACTGAAGCATCCAGTCTTGTGACTTCAATGATG 4492

RESULT 5
 AA25072
 ID AA25072 standard; cDNA; 5253 BP.
 XX AA25072;
 AC
 XX
 XX
 DT 09-DEC-1999 (first entry)
 XX
 DE Murine MEK1 nucleotide sequence.
 XX
 KM MEK1; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK;
 KM extracellular regulated kinase; signal transduction; regulation;
 KM MAPK/ERK; MEK; MKK; inflammation; cellular proliferation;
 KM differentiation; development; cell death; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 15..4496
 FT /tag= a
 FT /product= "MEK1"
 XX
 XX W09947686-A2.
 PD 23-SEP-1999.
 XX
 PF 15-MAR-1999; 99MO-US05556.
 XX
 PR 16-MAR-1998; 98DS-0078153.
 PR 04-SEP-1998; 98DS-0099165.
 XX
 PA (CADU-) CADUS PHARM CORP.
 PI Johnson GL.
 XX
 DR WPI: 1999-571843/48.
 DR P-PSDB: AAY42107.
 PT New human MEK polynucleotides and polypeptides, used for regulating
 PT signal transduction in cells -
 XX
 PS Example 1; Fig 3; 159pp; English.
 XX
 CC The present sequence encodes murine mitogen-activated protein kinase/
 CC extracellular response kinase (MAPK/ERK) kinase kinase (MEKK),
 CC specifically designated MEK1. The MEK proteins are used to modulate
 CC and regulate signal transduction in cells, as well as for regulation of
 CC gene transcription in a cell encoding MEK, where the cell is involved
 CC in inflammation, regulation of cellular proliferation and
 CC differentiation, regulation of development, regulation of cell death or
 CC regulation of inflammation. They are also used to prepare antibodies.

CC MEK polynucleotides can be used to produce the protein recombinantly
 CC and as a source of probes and primers.
 XX
 SQ Sequence 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 other;
 Query Match 65.1%; Score 3417; DB 20; Length 5253;
 Best Local Similarity 83.5%; Pred. No. 0;
 Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY 1 GAGAAATGAGCGGCGGCGGGAATCGGCTCGTCGCGGGAATCCCGGCGGCGAG 60
 DB 9 GAGAAATGAGCGGCGGCGGCGGGAATCGGCTCGTCGCGGGAATCCCGGCGGCGAG 68
 QY 61 GCTACGAGCCCTTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 111
 DB 69 GCGGCGGAGTCCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 128
 QY 112 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 168
 DB 129 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 188
 QY 169 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 228
 DB 189 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 248
 QY 229 GAGCAGCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 285
 DB 249 GAGCAGCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 308
 QY 286 GAGCAGCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 345
 DB 309 GAGCAGCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 368
 QY 346 CAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 405
 DB 369 CCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 428
 QY 406 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 465
 DB 429 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 458
 QY 466 TCTCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 525
 DB 459 CCTTCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 518
 QY 526 CACAAATGAGATGATGCTCCAGAGCAAGATGATGATGATGATGATGATGATGATGAT 585
 DB 519 CACAAATGAGATGATGCTCCAGAGCAAGATGATGATGATGATGATGATGATGATGAT 578
 QY 586 ATGCCAGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 645
 DB 579 ATGCCAGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 638
 QY 646 AAGCAATCCCGATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 705
 DB 639 AAGCAATCCCGATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
 QY 706 GAGAGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 765
 DB 699 GAGAGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 758
 QY 766 GCGGAGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 825
 DB 759 GCGGAGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 818
 QY 826 GTTCCCGAGTGGCTTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 885
 DB 819 GTTCCCGAGTGGCTTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
 QY 886 GATGCTTCTCAACATATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 945
 DB 879 GATGCTTCTCAACATATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 938

Db 3054 TGCTGGAACCGAGACTCAGACCAAGCTCTCCCAAGTCTTCACTAGTCAAGACCCCA 3113
 Qy 3163 CCTCCAGTAACATACACAGGCCAAGCCATCTAGACCTAACCCAGTAATACAGTAA 3222
 Db 3114 CCTCCAGTAACATACACAGGCCAAGCCATCTCCAGGAGTCCAGGAGTCAAGCAAA 3173
 Qy 3223 CAGGAGATCCCTCAAAAATAGCATGACATGATCTGACAGCTTGTCCAAATGTGAT 3282
 Db 3174 CTAGGGGAGCCACAAAAGATGACATGATCTGAGGAGTGTCCAGGTGTGAC 3233
 Qy 3283 GACAGCTTGGCTGTAGCAGCAATAGTAATGCTGTATATCCAGTACAGAGACGTG 3342
 Db 3234 GACAGCTTGGGGGGGGGGGCAACATGCGCAACGCCGTATACCCAGCCAGACAGT 3293
 Qy 3343 TTACCCCACTAGAGAGAGAAATGCAATGATGTCATACAGAGCTCAATCCAGTATT 3402
 Db 3294 TTACACCCCGGTGGAGCAAGTGCAAGTTAGATGTGACACCGAGCTCAACTCCACATC 3353
 Qy 3403 GAGGACCTCTTGAAGCACTATGCTTCAAGTATACAAAGTAACTTTTAAGTCAGAA 3462
 Db 3354 GAGGACCTCTTGAAGCACTATGCTTCAAGTATACAAAGTAACTTTTAAGTCAGAA 3413
 Qy 3463 GTTGTGCTCTCTCTCTGAAAAAGCTGAAAAATGATGATACCTACAAAGTGTGAAT 3522
 Db 3414 GTGCGCGTCTCTCTCTCGGAAAAAGCGGAAAAATGAGACACCTACAAAGCAGTCAAT 3473
 Qy 3523 CATTAATCAAAAGTCAAGAGAGATGAGAACTGAAAGAAAGAAAGCTTTAGCAATGGC 3582
 Db 3474 CATTAATCAAAAGTCAAGAGAGATGAGAACTGAAAGAGAGAGAGCTTTAGCAATGGC 3533
 Qy 3583 ATGGCAATGTACGCGTACAGAGATGCGCCATGCTTCCAGTGTGAGAGTGAAGAT 3642
 Db 3534 ATGGCAATGTACGCGTACAGAGATGCGCCATGCTTCCAGTGTGAGAGTGAAGAT 3593
 Qy 3643 GGAGAGATATCATCTATTTAAACAGATACACAGACACTCTACAGAGACATACAAA 3702
 Db 3594 GGAGAGATATTTATCATCTTACAGAGACACACCAAGAACTCTTCCAGAGACATACAAA 3653
 Qy 3703 GCAAAAACAACCTGATAGAGAGACACTGAAATGGCTGAAAGGTCAACAGATAGGCTTGA 3762
 Db 3654 GCGAAAACACCTTACAGAGAGACGCTGAGTGTGAAAGGCGCAGCATAGGCTCTGGA 3713
 Qy 3763 GCATTTCTCTCTTATGATAGGCTCAAGATGGGGAACGGAACCTTAATGGCTGTAA 3822
 Db 3714 GCATTTCTCTCTTATGATAGGCTCAAGATGGGGAACGGAACCTTAATGGCTGTAA 3773
 Qy 3823 CAGTGACTTATGTCAGAAAACATCTTCTGAGCAAGAAAGATAGAGCACTAAGA 3882
 Db 3774 CAGTGACTTATGTCAGAAAACATCTTCCGAGCAGAGAGAGGTGTGAGAGCTTGAAG 3833
 Qy 3883 GAAGAGATTAAGATATGAGCACTGAAATCATCCAAACATCTTAAGATTTGGAGCC 3942
 Db 3834 GAAGAGATCCGATGATGGTCACTCAACATCCAAACATCTCCGATGCGGGGGCC 3893
 Qy 3943 AGCTGAGAGAGCAATTAACAATCTCTCATTTGAATGGAGGGAGTGGTGGCT 4002
 Db 3894 AGCTGAGAGAGCAATTAACAATCTCTCATTTGAATGGAGGGAGTGGTGGCT 3953
 Qy 4003 CATTTGCTAGTAATATGAGCCTTCAAGAAATCAGTATTATTAATACATGAGAAC 4062
 Db 3954 CACCTCTTGAATTAATAGGAGCTTCAAGAGTGTGATTAATCACTACAGTGTGAG 4013
 Qy 4063 TTACTGCGTGGCTTGTATCTCCATGAAAACCAATCATTCACAGAGATGTCAAAAGT 4122
 Db 4014 TTACTGCGTGGCTTGTATCTCCATGAAAACCAATCATTCACAGAGATGTCAAAAGT 4073
 Qy 4123 GCCAATTTGCTAATTAAGCACTGTCAGAGACTTAAGAAATTTGAGACTGCA 4182
 Db 4074 GCCAATTTGCTAATTAAGCACTGTCAGAGACTTAAGAAATTTGAGACTGCT 4133
 Qy 4183 GCCAGTTGGCATCAAAAAGAACTGGTCAGAGAGATTTCAAGGACATTAATCTGGGACA 4242
 Db 4134 GCCAGTTGGCATCAAAAAGAACTGGTCAGAGAGATTTCAAGGACATTAATCTGGGACA 4193

Qy 4243 ATTGCATTTATGGCACTGAGTACTAAGAGTCAACAGTATGGAAGAGCTGTGATGA 4302
 Db 4194 ATTGCATTTATGGCACTGAGTACTAAGAGTCAACAGTATGGAAGAGCTGTGATGA 4253
 Qy 4303 TGGAGTGTGGCTGTCTATTAAGAAATGGCTTGTGCAAAACACCATTAAGATGCAAG 4362
 Db 4254 TGGAGTGTGGCTGTCTATTAAGAAATGGCTTGTGCAAAACACCATTAAGATGCAAG 4313
 Qy 4363 AAACATCCAAATCATCTTCTGATTAATTAAGATGATGATGATGATGATGATGATGATG 4422
 Db 4314 AAACATCCAAATCATCTTCTGATTAATTAAGATGATGATGATGATGATGATGATGATG 4373
 Qy 4423 ATCCCTTCAATTTGCTCTGCTGTTTACAGAGATGAGCTCTTCTGTTTGAATTCGA 4482
 Db 4374 ATCCCTTCAATTTGCTCTGCTGTTTACAGAGATGAGCTCTTCTGTTTGAATTCGA 4433
 Qy 4483 CCTCAGAGACAGACCTCCATCAAGAGAGCTGATGAAACATCCAGTCTTCTGTTTGAATTCGA 4542
 Db 4434 CCTCAGAGACAGACCTCCATCAAGAGAGCTGATGAAACATCCAGTCTTCTGTTTGAATTCGA 4493
 Qy 4543 TAGCCATTTATGAGATCAACTACATGATGATGATGATGATGATGATGATGATGATG 4602
 Db 4494 TAGCCATTTATGAGATCAACTACATGATGATGATGATGATGATGATGATGATGATG 4553
 Qy 4603 TG---TGGGGAACCAATTTATTTCTACTGCAATGATGCCATGAAACAGCTATGAAC 4658
 Db 4554 AGAACTTGTGGGGGACCATGCGCTTAACCGCAGCCCTCAGCCATGAAACAGCAGCAAAAC 4613
 Qy 4659 GAGGCGAGTGGGGGACCTTACTAGTATGATGATGATGATGATGATGATGATGATGATG 4718
 Db 4614 GAGGCGAGTGGGGGACCTTACTAGTATGATGATGATGATGATGATGATGATGATGATG 4672
 Qy 4719 CTCAGATGCA-AAAGCCCAAACTAGTGAAGAACTGTAAGTCTCTTCAAAAGT 4777
 Db 4673 CTCAGATGCAAGATCTACAGTCTGATGATGATGATGATGATGATGATGATGATGATG 4732
 Qy 4778 GGCCTAGTGAACAGAAACAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATG 4837
 Db 4733 GGCCTAGTGAACAGAAACAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATG 4792
 Qy 4838 TATTTTGGAGCACTTTTTCAGCA 4864
 Db 4793 TA--TTTGGAGCACTTTTTCAGCTA 4817

RESULT 6
 AAX80911
 ID AAX80911 standard; cDNA; 5253 BP.
 XX AAX80911;
 AC 03-NOV-1999 (first entry)
 DT 03-NOV-1999 (first entry)
 XX Murine MEK1 cDNA.
 DE Murine MEK1 cDNA.
 XX Murine MEK1 cDNA; Mitogen ERK kinase 1 protein; MEK1; proteinase;
 KW extracellular signal regulated kinase; ERK; signal transduction pathway;
 KW regulation; apoptosis; protein kinase; cleavage; caspase; antibody;
 KW kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection;
 KW immunoreactive; diagnostic; therapeutic assay; reagent; disorder;
 KW aberrant expression; activation; MEK1 gene product; DNA probe; primer;
 KW selectively hybridise; ss.
 OS Mus sp.
 XX
 FH key location/Qualifiers
 FT CDS 15..4496
 FT /tag- a
 FT /product- "MEK1 protein"
 FT /function- "Regulates cellular apoptosis"
 FT 5'UTR 1..14
 FT /tag- b

FT 3'UTR 4497..5253
FT mat-peptide 2637..4493
FT /*tag= c
PN /note= "Active fragment that mediates apoptosis"
XX MO9941385-A1.
XX
XX
XX 19-AUG-1999.
XX
XX 12-FEB-1999; 99MO-US02974.
XX
XX 13-FEB-1998; 98US-0023130.
XX
XX (CADU-) CADUS PHARM CORP.
XX
XX Johnson GL;
XX
XX WPI: 1999-508649/42.
XX
XX P-PSDB: AAY26234.
DR
PT A new mammalian serine-threonine protein kinase for treating
PT disorder characterized by aberration of the enzyme gene
XX
XX
PS Claim 1a: Page 113-119; 149pp; English.
XX
XX The present sequence is an isolated murine MEK1 cDNA. It encodes
CC Mitogen ERK kinase 1 (MEK1) protein, which functions to
CC integrate proteases and signal transduction pathways involved in the
CC regulation of apoptosis. It is a 196 kDa protein kinase, which upon
CC cleavage at Asp 871/874 by caspase generates a 91 kDa kinase fragment
CC that induces apoptosis and a 113 kDa NH2-terminal fragment. Mutant MEK1
CC proteins that are resistant to cleavage by caspase proteases and capable
CC of inhibiting apoptosis can be produced. MEK1 proteins and antibodies
CC immunoreactive with MEK1 are used in diagnostic and therapeutic
CC assays and reagents for detecting and treating disorders involving
CC aberrant expression or activation of the MEK1 gene products. DNA probes
CC or primers that selectively hybridise to MEK1 cDNA, can be used for its
CC detection in samples.
XX
SQ Sequence 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 other;

Query Match 65 18; Score 3417; DB 20; Length 5253;
Best Local Similarity 83.58; Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY 1 GAGAAATGCGCGCGCGGGAATCGCCTGCTGTCGGGATTCCCGGCGCAGG 60
DB 9 GAGAAATGCGCGCGCGGCGGATCGCCTGCTGTCGGGATTCCCGGCGCAGG 68
QY 61 GCTACGAGCCCTGAGCGAGCGCGGCGC-----GGAGAGCCCTCAAGCGAGCAGC 111
DB 69 GCGCGCGAGTCCCGAGCGCGCGCGCGGCGAGAGAGAGAGAGCTCCAGGAGAGCGCC 128
QY 112 GCGCGC---GCGGCTGCGCGGAGCTGCTGCGGAGCGGCGAGCGCGGCGGAGG 168
DB 129 GCGCGCGCGAGCGCGCGCGGCGGCTGCTGCGGAGCGCTGCGAGCGCGCGGAGCGC 188
QY 169 GCGGACTGCGCGCGCGCGAGCTGCGCAAAAGTGGAGTGGAGCTGGAGCAGCTGCT 228
DB 189 GCGGACTGCGCGCGCGCGGCGGACGTGCGCAAAAGTGGAGTGGAGCTGGAGCAGCTGCGG 248
QY 229 GAGCAGCGCTCTCTCTGCGCGCTCAACCGCGGCT---CCTGACTTCCCGTGGCG 285
DB 249 GAGCAGCGCTCTCTCTGCGCGCTGCGCGCTGCGCGCTGCGCATCTCTCTCTGCGCG 308
QY 286 GAGCGCGCGGAGCGAGGAGGAGTGGAGCGGCTTCCAGCCTGAGGCTGCGCGCGCGCGCC 345
DB 309 GAGCGCGCGGAGCGAGTGGAGGAGCTGCTTCCAGCGCGCGCGGAGCGCGCGCACCC 368
QY 346 CAGCAGCGCGGAGCG 405
DB 369 CCGGAGCGCGGAGCTGCGCTGCGGCTCCACCTCTCCGAGCTGGGCGCGCGCGGAGCAGC 428

QY 406 GCGCGCTGAGTCCCGCAGCGCGCGAGCGCGGAGAAAGCGGCGCGCGCGCGGAGCGC 465
DB 429 GCGCGCGCGAGCGCGCGCGG-----GCCGAGCGC 458
QY 466 TCTCCTGAGCGCGCGCGCGGCTGCGAGTGGAGTAAGAACTCTCAAGAGCTG 525
DB 459 CCTCTGAGCGCGCGCGCGCGGCTGCGAGATGGAGTAAGAACTCTCAAGAGCTG 518
QY 526 CACAAGATGATGATGCTGTCAGAGGAACGATGATCAGGAGAACTCAAGCAGCTGT 585
DB 519 CACAAGATGAGAGATGCGCGCGGAGAGAGATGATCAGGAGAACTCAAGCAGCTGT 578
QY 586 ATGCGAGCTGGAAGCAGCAATGGTGGAAAGAGAAATAGCGAGGCTGTGGTGTGA 645
DB 579 ATGCGCGCGCTGGAAGCAGCAATGGTGGAGAGAGAGAGAGAGGCGCTGTGGTGTGA 638
QY 646 AAACCAATCCAGTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 705
DB 639 AAGCCATCCCTATTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
QY 706 GAGAGCTCCAGGCAAGCGCGCTTCCAGCAGCTTCCAAAGCGCGAGCTCTCTCTCT 765
DB 699 GAGAGGCGCGAGCAGCTTCCGCTCCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 758
QY 766 GGCACCTCCCATGAGTGCAGCAGTGAATCAGATCTCCAGAGTAAAGAGAAAGA 825
DB 759 GCGAGCTCTCGTACAGCGCGCTCGGTGAAGCGGAATCCCGAGAGTAAAGCGAAAGA 818
QY 826 GTTTCGCCAGTGCCTTTTCAAGTGGAGATACACACCGCGGAGAGCGCGCTTCAACA 885
DB 819 GTTTCGCCAGTGCCTTTTCAAGTGGAGATACACACCGCGGAGAGCGCGCTTCAACA 878
QY 886 GATGCGCTTCCATATATAGCTTGAAGAAACCGCGGTGAAGAGTGAATGATGATG 945
DB 879 GATGCGCTTCCATATATAGCTTGAAGAAACCGCGGTGAAGAGTGAATGATGATGATG 938
QY 946 GCCAGCTTACTTACTGACAGATGAGGCTTAACTCTTCTGATTTGAGAGAGCAGC 1005
DB 939 GCCAGCTTACTTACTGACAGATGAGGCTTAACTCTTCTGATTTGAGAGAGCAGT 998
QY 1006 CCAGCAATTAATACCGGCTTTTATTTGGGCTCAGAACTGAGTGCAGCTGAGCA 1065
DB 999 CCAGCAATTAATACCGGCTTTTATTTGGGCTCAGAACTGAGTGCAGCTGAGCA 1058
QY 1066 TTCTGTATTCATGCTGCTTATTTGATGCTCGGCGGCTTCAACCTTGAACCTTCAACCCA 1125
DB 1059 TTCTGTATTCATGCTTCTTGTGCTGCTCGGCGGCTTCAACCTTGAACCTTGAACCCA 1118
QY 1126 ATGTTATGAGAAATCTTTAAAGATTTGAGGTTGAGAGTTGTTCCAGAAATATAC 1185
DB 1119 ATGTTATGAGAAATCTTTAAAGATTTGAGGTTGAGAGTTGTTCCAGAAATATAC 1178
QY 1186 AGTAGGCTTACTCAAGATCAAAAGCTTCATCTGTAACACATCCAAAGATTTGTTCA 1245
DB 1179 AGTAGGCTTACTCAAGATCAAAAGCTTCATCTGTAACACATCCAAAGATTTGTTCA 1238
QY 1246 CGCATGTCAAATTTCTAATACATTTGATCATCATCTAGTCTAGTCTAGTCTAGTCTAGTCT 1305
DB 1239 CGCATGTCAAATTTCTAATACATTTGATCATCATCTAGTCTAGTCTAGTCTAGTCTAGTCT 1298
QY 1306 AGCATTAAGATGAGAGAGAAACAGATGCTCTATTTGCTGTTGGGAGTGGTGA 1365
DB 1299 AGCATTAAGATGAGAGAGAAACAGATGCTCTATTTGCTGTTGGGAGTGGTGA 1358
QY 1366 GAAAGCTTACAGTGTGAGAGAGCGGCGGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1425
DB 1359 GAAAGCTTACAGTGTGAGAGAGCGGCGGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1418
QY 1426 ATTTGGGAGAGAGAGTGAAGAAATAGAAACCTTTAATATGCTCTTGTGATCT 1485
DB 1419 ATTTGGGAGAGAGTGAAGAAATAGAAACCTTTAATATGCTCTTGTGATCT 1478

0Y 1486 AAGTGGAGATCTCATGATTTCTACAGCCAGAGTGTCAAGTCTCTGATTTCCCTTC 1545
Db 1479 AAGTGGAGATCCCATGATCTTACAGCCATGATTTATCAAGCCCTCGGTGATCCCCGCC 1538
0Y 1546 TCCCTGAGAGCTGCACAGCAGCAAAACGATACAGCAGAGCTTTGGCTGGATCA---CGA 1602
Db 1539 TCCCTGAGAGCTGTCCAGCAGCCATCTCCCGCAGCAGCCCTGGCGGATACAGCCGG 1598
0Y 1603 AAGATCAAGAGACAAATTTTAACTTACTCATTTATGAACTCAGAAATCCCTCTGCT 1662
Db 1599 AAGAAATCAGAGAGCAGTTTAACTTACTCATTTTGGAAACCCAGAGATTCCTTCCGCT 1658
0Y 1663 TCAAAAGATTTAGCTGAGCCATGAGATTCAGTGTGGTGAAGTGAAGTCCGCTGCTTA 1722
Db 1659 TCAAAAGATTTGCGAGCCATGAGATTCAGTGTGGTGAAGTGAAGTCCGCTGCTTA 1718
0Y 1723 TTTTCTAGAAACTGGAATGTGAGAGAGATGAGCCCTCAGCCGCTTCCCATGATGTCAGT 1782
Db 1719 TTTCTAGAAACTGGAACGTAAGGGAATGAGCCCTTAGCGCTTTCCTCAGCAGCTTACG 1778
0Y 1783 GGGGCCCTCTGTTGGCAAAATGGGAGAGACACTGGAATTTCTGGGGCAGCAGTGGAAAC 1842
Db 1779 GGGGCCCTGTTGTGGCAAAACGGGGAGAGACACTGGAATCTTGGAGCGGCACTGGGGGC 1838
0Y 1843 AGCCGAGTGGGGAGCCACAGTGGTCTTCCAGACCCAGTATCTCAGGAGATGTTGTTG 1902
Db 1839 AGCTTAAGCGCGGAGCGCCAGCGGGTCTCCAGCCCAAGCATCTCAGGGAGATGTTGTTG 1898
0Y 1903 GAGGACTGCTGAGCGCTTCTCATAGTCTGCTGCTGACCCGCTGTACAAAGTATGACGTT 1962
Db 1899 GAGGCTGCTGAGCGTCTCTGCTCATAGTCTGCTGCTGACCCGCTGTACAAAGTATGACGTT 1958
0Y 1963 GCTGCTTTAAAAACATTTGAGAGCATGCTGTATACATCTTGGCCACAGTCTGGAGAA 2022
Db 1959 GCTGCTTTAAAAACATTTGAGAGCATGCTGTATACATCTTGGCCACAGTCTGGAGAA 2018
0Y 2023 AGAATCAAACTTCAGAGACTTCTCCAGCCAGTGTAGAGACCACTCCCTAGTCAATTTGCA 2082
Db 2019 AGAATCAAACTTCAGAGACTTCTCCAGCCAGTGTAGAGACCACTCCCTAGTCAATTTGCA 2078
0Y 2083 GATGCCAATAGCCGACAGTACAGTGTCCATATCAACACTGTTGGAACTGTGCAAAAGC 2142
Db 2079 GATGCCAATAGCCGACAGTACAGTGTCCATATCAACACTGTTGGAACTGTGCAAAAGC 2138
0Y 2143 CAAGCAGGAGAGTGGCAGTGGCAGAGAAATCTTAAAGCTGTGATTTGGT 2202
Db 2139 CAAGCAGGAGAGTGGCAGTGGCAGAGAAATCTTAAAGCTGTGATTTGGT 2198
0Y 2203 GGTGTTGATTTATGTCTTAAATGTATTTCTTGAACCAAACTGAATCAAAATTTGCCAA 2262
Db 2199 GGTGTTGATTTATGTCTTAAATGTATTTCTTGAACCAAACTGAATCAAAATTTGCCAA 2258
0Y 2263 GAACCTCTTGGCCGCTTTGTCTTATAGATAGACTGTGTGGAAATTTCTGCTGTAATTT 2322
Db 2259 GAACCTCTTGGCCGCTTTGTCTTATAGACAGGTTGCTGTGGAAATTTCTGCTGTAATTT 2318
0Y 2323 TATCTCATATTTGTAGTACTGATGTTTACAAAGCTGAGCCCTGTTGAAATCAGGTATAG 2382
Db 2319 TATCTCATATTTGTAGTACTGATGTTTACAAAGCTGAGCCCTGTTGAAATCAGGTATAG 2378
0Y 2383 AAGCTGCTTCCCTTTAATCTTTGCTTTCAGTCCATTTGATTAATTTCCACATCAATGGTT 2442
Db 2379 AAGCTGCTTCCCTTTAATCTTTGCTTTCAGTCCATTTGATTAATTTCCACATCAATGGTT 2438
0Y 2443 GGCATAACTTCCAGAGATGATCTAGTGTCTGCAAGATGTTTACTACAGTATCCCAT 2502
Db 2439 GGCATAACTTCCAGAGATGATCTAGTGTCTGCAAGATGTTTACTACAGTATCCCAT 2498
0Y 2503 GTGTTTTCAAAACCTGTTAGAAAATGCTGAGTGTTCAGATTTCCACTGACCTTACACAGATG 2562
Db 2499 GTGTTTTCAAAACCTGTTAGAAAATGCTGAGTGTTCAGATTTCCACTGACCTTACACAGATG 2558
0Y 2563 GCTCGCGCTTTGATGGCTTTTGCAGATGAGGTGGAATTTGCCCAAGCCATCCAGTTGGCG 2622

Db 2559 CGCGGGCGTCTGATGGCTATCGGGATGAGTGGAAATTTCCAGGCTACACAGCTGGGT 2618
0Y 2623 GTAGAGACACTTTGGATGGTCAACAGAGACGCTTCTTGGCAGCATCTGTTCCCAACAC 2682
Db 2619 GTGAGAGACACTTGGATGGTCAACAGAGACGCTTCTTGGCAGCATCTGTTCCCAACAC 2675
0Y 2683 TATCTGAAAACACAGAGAACATTCCTTGAAGTGCACAGTCCATTTAGAGAAACTGGA 2742
Db 2676 TATCTGAAAACACAGAGAACATTCCTTGAAGTGCACAGTCCATTTAGAGAAACTGGA 2726
0Y 2743 AAGGATTAATGCTTCAAAATGATGGCCATTCAGAGAGACATTTCTGAGAACCTGGCC 2802
Db 2727 AAGGATTAATGCTTCAAAATGATGGCCATTCAGAGAGACATTTCTGAGAACCTGGCC 2786
0Y 2803 AGCATTTAGTAGACCTTCTTACTTCAACAAACAAACAAACAAACAAACAAACAAACCA 2862
Db 2787 GGGCTCTCTGTAGACTTCTCCACT-----CAACAAACAAACAAACCA 2831
0Y 2863 AAGCCAAATGGTCAAAACAAAGCAGACCCACAGTCAAGTGTGAACTCTCTCTTTA 2922
Db 2832 AAGCCAGCGGTTCAAAACAAAGCAGACCCACAGTCAAGTGTGAACTCTCTCTTTG 2891
0Y 2923 TCTCATCATTCCTCAATTAATGTTTCCAGCTTTCACACCCCTTCTTCTTACCCATCT 2982
Db 2892 TC---TCACTCAATTAATGTTTCCAGCTTTCACACACACACACCCCTTCTTCTTACCCATCT 2948
0Y 2983 GTACCAAGCTGGCACTGCAACAGATGCTCTCAACATTAAGATTTCAATTTCCCTG 3042
Db 2949 GTCC-----CAGATATTTCTAACACAGACAGACCCAGGATTTGTTCCCTGC 2993
0Y 3043 AGAATACCTTCTGCACTCTCTCAACACAGCGCAAGTTTCTGTACAAATTCACAGAAC 3102
Db 2994 AATATACCTTCTGCACTCTCTCAACACAGCGCAAGTTTCTGTACAAATTCACAGAAC 3053
0Y 3103 TGTCTGAAAACAAAGACTAGATAAATTTCCCGAGTCTTCTAGTCAACACCTTGC 3162
Db 3054 TGTCTGAAAACAAAGACTAGATAAATTTCCCGAGTCTTCTAGTCAACACCTTGC 3113
0Y 3163 CCTCCAGTACATACACAGGCGCAAGCCATCTAGACCTTACCCAGATTAATCAAGTAA 3222
Db 3114 CCTCCAGTACATACACAGGCGCAAGCCATCTAGACCTTACCCAGATTAATCAAGTAA 3173
0Y 3223 CAGGAGATCTCTCAAAAATTAACATGACACTTGATCTGACAGTATGTTTCAAAATGAT 3282
Db 3174 CAGGAGATCTCTCAAAAATTAACATGACACTTGATCTGACAGTATGTTTCAAAATGAT 3233
0Y 3283 GACAGCTTGGCGTGTAGCAGCAATAGATAATGCTTATACCCAGTGCAGAGATG 3342
Db 3234 GACAGCTTGGCGTGTAGCAGCAATAGATAATGCTTATACCCAGTGCAGAGATG 3293
0Y 3343 TTAGCCCAAGTAGAGAGAAATGAGATTTAGATGTCAATACAGAGCTCAACTCAGTAT 3402
Db 3294 TTAGCCCAAGTAGAGAGAAATGAGATTTAGATGTCAATACAGAGCTCAACTCAGTAT 3353
0Y 3403 GAGGACCTTCTTAAACATCTATGCTTCAAGTATCAACAGTAATTTTAAAGTCAAA 3462
Db 3354 GAGGACCTTCTTAAACATCTATGCTTCAAGTATCAACAGTAATTTTAAAGTCAAA 3413
0Y 3463 GTTGTGCTCTGTCTCTGAAAAGGCTGAAAAGATGATACCTACAAAGATGATGGAT 3522
Db 3414 GTTGTGCTCTGTCTCTGAAAAGGCTGAAAAGATGATACCTACAAAGATGATGGAT 3473
0Y 3523 CATATTAACAAAGTGCAAAGAGATGAGATGAGAGTGAAGAGAAAGATTTAGCAATTTGCC 3582
Db 3474 CATATTAACAAAGTGCAAAGAGATGAGATGAGAGTGAAGAGAGAGAGCTTTAGGATTCGCC 3533
0Y 3583 ATGGCAATGTCAAGCTCTCAGATGCTCCCTCCCATATGTTCTCAGCTGCAAGTTGAAAT 3642
Db 3534 ATGGCAATGTCAAGCTCTCAGATGCTCCCTCCCATATGTTCTCAGCTGCAAGTTGAAAT 3593
0Y 3643 GAGAGATATATCATTTATTTACAGAGATACCCAGAGACTTACCAGAGACTTACAAA 3702

DB 3594 GGAAGATATTTATCATTCATTCAGCAGACACACAGAAACTCTTCCAGCATATACCAA 3653
QY 3703 GCAAAACACCCGTATAGAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTGA 3762
DB 3654 GCGAAACAGCCTTACAGAGAGAGCGGTGAGTGAAGGACAGAGATAGGCTTGA 3713
QY 3763 GCATTTTCTTCTGTTATATCAGGCTCAAGATGAGGAACTGGAACCTTAAATGCTTTAA 3822
DB 3714 GCATTTTCTTCTGTTATATCAGGCTCAAGATGAGGAACTGGAACCTTAAATGCTTTAA 3773
QY 3823 CAGTGCATATGTCAGAAACACATCTTTCAGCAAGAAAGATAGAGCACTAGA 3882
DB 3774 CAGTGCATATGTCAGAAACACATCTTTCAGCAAGAAAGATAGAGCACTAGA 3833
QY 3883 GAAGAGATTAAGATGATGAGCCTGATCATCATCAAAACATCATTTAGATGTTGGAGCC 3942
DB 3834 GAAGAGATCGGATGATGAGTGCATCATCAACATCAAAACATCATTCGGATGCTGGGCC 3893
QY 3943 ACCTGAGAGAGACAAATTAATCTCTTCATTTGATGATGCGAGGGGATCGTGCT 4002
DB 3894 ACCTGAGAGAGAGACAACTCAACCTCTTCATTTGATGATGCGAGGGGATCGTGCT 3953
QY 4003 CATTTGCTGATTAATTAAGAGCTTCAAGAAATCAGTATTAATTAATTAATTAATTA 4062
DB 3954 CACCTCTTGTGATTAATTAAGAGCTTCAAGAGCTGCTCATTAATTAATTAATTAATTA 4013
QY 4063 TTACTCGTGGCTTCTGATCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4122
DB 4014 TTACTCGTGGCTTCTGATCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4073
QY 4123 GCCAATTTGCTAATTAAGAGCTGCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4182
DB 4074 GCCAATTTGCTAATTAAGAGCTGCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4133
QY 4183 GCCAGGTGGCATCAAAAGAGACGTCGAGAGAGTTTGAAGGACAAATTAAGGAGGACA 4242
DB 4134 GCCAGGTGGCATCAAAAGAGACGTCGAGAGAGTTTGAAGGACAAATTAAGGAGGACA 4193
QY 4243 ATTGCAATTAAGAGCTGCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4302
DB 4194 ATTGCAATTAAGAGCTGCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4253
QY 4303 TGGAGTGTGCTGCTGATTAATTAAGAGCTGCTCATGAAACCAATCATTCACAGAGAT 4362
DB 4254 TGGAGTGTGCTGCTGATTAATTAAGAGCTGCTCATGAAACCAATCATTCACAGAGAT 4313
QY 4363 AAACAGTCCAAATCATCTGCTTGAATTAAGAGCTGCTCATGAGATGCTGCATCG 4422
DB 4314 AAACAGTCCAAATCATCTGCTTGAATTAAGAGCTGCTCATGAGATGCTGCATCG 4373
QY 4423 ATCCCTTCAATTTGCTGCTGTTTACGAGATGAGCTCTGCTGTTTGAAGACTTCAA 4482
DB 4374 ATCCCTTCAATTTGCTGCTGTTTACGAGATGAGCTCTGCTGTTTGAAGACTTCAA 4433
QY 4483 CCTCAGAGACAGCTCCTCATGAAGAGCTGCTCATGAGATGCTGCATCG 4542
DB 4434 CCTCAGAGACAGCTCCTCATGAAGAGCTGCTCATGAGATGCTGCATCG 4493
QY 4543 TACCAATTTGAGATCAATCAAGTAAAGAGATGCTCATGAAGAGATGCTGCATCG 4602
DB 4494 TACCAATTTGAGATCAATCAAGTAAAGAGATGCTCATGAAGAGATGCTGCATCG 4553
QY 4603 TG----TGAGGAACCAATGATTTCTTACCTGAGATGCTCATGAAGAGATGCTGCATCG 4658
DB 4554 AGAAGTGTGGGGGACATCGCGTAAACGAGCGCTCAAGCAGCATTAACAGCAAGAAC 4613
QY 4659 GAGGCCAGTGGGGAACCCCTTACTAGTATGATGATGATGATGATGATGATGATGATGATG 4718
DB 4614 GGGGCGCGCGGGGAA--CCGATCTCAACATGATGATGATGATGATGATGATGATGATGATG 4672
QY 4719 CTCAGTATGCA--AAAGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATG 4777
DB 4673 CTCAGTATGCAATCTTACAGCTCGTGCAGAGATGCTCAACAGCTCGTGCATTCACAGAGAT 4732

QY 4778 GGCCTAGTGAACAGGAAACATGAATGATGATGATGATGATGATGATGATGATGATGATG 4837
DB 4733 GGCCTAGTGAACAGGAAACATGAATGATGATGATGATGATGATGATGATGATGATGATG 4792
QY 4838 TATTTTGGAGCCTTTTTCAGCAA 4864
DB 4793 TA--TTTTGGAGCCTTTTTCAGCTA 4817

RESULT 7
AAL41578
ID AAL41578 standard; cDNA; 5539 BP.
XX
AC AAL41578;
XX
DT 19-APR-2002 (first entry)
XX
DE Murine MEK1-2 coding sequence.
XX
KW Mouse; MEK1; mitogen ERK kinase; enzyme; cancer; neuroprotective;
KW autoimmune disease; signal transduction; allergy; inflammation;
KW neurological disorder; hormone-related disease; apoptosis; infection;
KW cytosolic; immunosuppressive; antiinflammatory; antiallergic; gene;
KW neotrophic; antiparkinsonian; contraceptive; ss.
XX
Mus musculus.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 1..4782
FT /tag= a
FT /product= "MEK1.2"
XX
PN US6333170-B1.
XX
PD 25-DEC-2001.
XX
PE 05-APR-1996; 96US-0628829.
XX
PR 15-APR-1993; 93US-0049254.
PR 14-OCT-1994; 94US-0323460.
PR 12-MAY-1995; 95US-0440421.
PR 06-JUN-1995; 95US-0472934.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Johnson GL;
XX
DR WPI: 2002-163179/21.
DR P-PSDB; AAM48935.
XX
PT New isolated nucleic acid encoding mitogen extracellular
PT signal-regulated kinase kinase, useful for gene therapy of e.g. cancer
PT and for recombinant protein production
XX
PS Claim 2; Column 111-122; 125bp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of murine mitogen extracellular signal-regulated kinase (ERK)
CC kinase kinase (MEK) enzymes. The sequences can be used to treat a wide
CC range of diseases including cancer, autoimmune diseases, inflammation,
CC allergies, degenerative neurological diseases and hormone-related
CC diseases, and for inhibiting spermatogenesis or oocyte maturation for
CC contraception. The present sequence is the murine MEK1.2 coding
CC sequence.
XX
SQ Sequence 5539 BP; 1320 A; 1559 C; 1515 G; 1145 T; 0 other;
Query Match 64.6%; Score 3387.6; DB 24; Length 5539;
Best Local Similarity 83.4%; Pred. No. 0;
Matches 4075; Conservative 0; Mismatches 709; Indels 102; Gaps 16;
QY 1 GAGAAATGGCGCGCGCGGGAATCGCCCTGCTGTCGGGATTCGCGGCGGCCAGG 60

QY 2204 GTGTTAATATGCTTAATATGATCTTGGAAACCAACTGATCAACATTTGGCAG 2263
DB 2486 GTGTCATTAACGCTTAAGTTGATCTTGGAAACCAAGCTGAATCAACAACTGGCCAG 2545
QY 2264 AACTTCTGGCCGCTTGTCTATAGATAGATGTTGTGGAAATTTCCGCTGAAATTT 2323
DB 2546 AACTGCTGGGTGCGCTGTCTATATAGACAGGTGTGCTGGAAATTTCCGCTGAAATTT 2505
QY 2324 ATCCATATTTGTCACTAGTATGTTTCAACAGCTAGCTGCTTGAATCAGTATAGA 2383
DB 2606 ATCCATATTTGTCACTAGTATGTTTCAACAGCTAGCTGCTTGAATCAGTATAGA 2665
QY 2384 AGCTGCTGCCCTTTAACCCTTGTGCTTGCATGATGATTAATTCCTCAATAGGTTG 2443
DB 2666 AGCTGCTGCCCTTTAACCCTTGTGCTTGCATGATGATTAATTCCTCAATAGGTTG 2725
QY 2444 GCAAACTTCCAGAAAGATCTAGTATGTTTCCAGAAAGTGTACTACAGTACCCATG 2503
DB 2726 GCAAGCTCTCTGGAGGATATATCTAGCTCTCCAGGATGTGACCGCGCTGCCGCTG 2785
QY 2504 TGTTTTCAAAACCTGTTAAGAAATGCTAGTGTTCAGTTTCACTCACTTCCAGAGATG 2563
DB 2786 TGTTTTCAAGCTGTATACCATCTTAATGCTTCTGCTCCACCCACTTCCAGAGATG 2845
QY 2564 GTCCGCTTTGATGCTATTTGCAAGATGAGGTGAATTTGCCGAAGCCATCAGTTGGCG 2623
DB 2846 GCGGCGGTGATGCTATGCTATGCGGATGAGGTGAATTTGCCGAGTCACTCAGCTGGGTG 2905
QY 2624 TGAAGACACTTGTGATGCTGCAACAGACAGCTTCTTGACGAGATCTGTTCCCAACAT 2683
DB 2906 TGAAGACACTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2962
QY 2684 ATCTGAAACACAGACAGATGCTTCCCTGAGTGCACAGTCCATTTAGAGAAACCTGAA 2743
DB 2963 GTCT-----AGAAACAGCTTCCCTGAGGATGAGGATGAGGATGAGGATGAGG 3013
QY 2744 AAGGATTAATGCTTACAAATTAATGATGCTTCAAGATGAGGATGAGGATGAGGATG 2803
DB 3014 AAGGATTAATGCTTACAAATTAATGATGCTTCAAGATGAGGATGAGGATGAGGATG 3073
QY 2804 GCATTCAGTATGAGGATGCTTCAAGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2863
DB 3074 GCATTCAGTATGAGGATGCTTCAAGATGAGGATGAGGATGAGGATGAGGATGAGGATG 3118
QY 2864 AGGCAATGTTTCAAAACAAAGGAGACCCAGCTAGTGTGAACTCTCTCTCTTAT 2923
DB 3119 AGGCAATGTTTCAAAACAAAGGAGACCCAGCTAGTGTGAACTCTCTCTCTTAT 3178
QY 2924 CTCATATTCCTCAATTAATGTTTCAAGCTTGTCAACCCCTTCTTCTTCAACCCATCTG 2983
DB 3179 C---TATGCTCAATTAATTTTCCAGACATCAGCCCTGTTCCCTGCCCCGCTG 3235
QY 2984 TACCAGCTGGCACTGCAACAGATGCTTCAAGATGAGGATGAGGATGAGGATGAGGATG 3043
DB 3236 TCC-----CAGATTAATTTTCAAGACAGCCAGGCTTGTGTTCCCTGCA 3280
QY 3044 GAATTAATTTGCTTCAATTAATGTTTCAAGCTTGTCAACCCCTTCTTCTTCAACCCATCTG 3103
DB 3281 AATTAATTTGCTTCAATTAATGTTTCAAGCTTGTCAACCCCTTCTTCTTCAACCCATCTG 3340
QY 3104 GTCTTCAAAACAAAGCTGATTAATTTTCCAGCTTGTCTTCACTCACTCAAGCCCTTGC 3163
DB 3341 GTCTTCAAAACAAAGCTGATTAATTTTCCAGCTTGTCTTCACTCACTCAAGCCCTTGC 3400
QY 3164 GCTTCAAAACAAAGCTGATTAATTTTCCAGCTTGTCTTCACTCACTCAAGCCCTTGC 3223
DB 3401 GCTTCAAAACAAAGCTGATTAATTTTCCAGCTTGTCTTCACTCACTCAAGCCCTTGC 3460
QY 3224 AGGAGATGCTTCAAAACAAAGCTGATTAATTTTCCAGCTTGTCTTCACTCACTCAAGCCCTTGC 3283
DB 3461 TACGAGGATGCTTCAAAACAAAGCTGATTAATTTTCCAGCTTGTCTTCACTCACTCAAGCCCTTGC 3520

QY 3284 ACACTTTGGCTGTACAGCAATAGTATGATGCTTATACCAAGTACAGAGACAGTGT 3343
DB 3521 ACAGCTTTGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3580
QY 3344 TCACCCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3403
DB 3581 TCACCCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3640
QY 3404 AGGACCTTCTTGAAGATCATGATGCTTCAAGTATACAAAGTAACTTTAACTGAGAA 3463
DB 3641 AGGACCTTCTTGAAGATCATGATGCTTCAAGTATACAAAGTAACTTTAACTGAGAA 3700
QY 3464 TTGCTGTCTGTCTCTGAAAGAGCTGAAATGATGATGATGATGATGATGATGATGATG 3523
DB 3701 TTGCTGTCTGTCTCTGAAAGAGCTGAAATGATGATGATGATGATGATGATGATGATG 3760
QY 3524 ATATCAAAAGTCAAAAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 3583
DB 3761 ATATCAAAAGTCAAAAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 3820
QY 3584 TGGCAATGTCAGGCTGTACAGATGCTTCCCATATGCTTCTCACTGCTGAGGATGAGG 3643
DB 3821 TGGCAATGTCAGGCTGTACAGATGCTTCCCATATGCTTCTCACTGCTGAGGATGAGG 3880
QY 3644 GAGAGATATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3703
DB 3881 GAGAGATATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3940
QY 3704 CAATAACAGCTTATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 3763
DB 3941 CAATAACAGCTTATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 4000
QY 3764 CATTTTCTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3823
DB 4001 CATTTTCTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4060
QY 3824 AGTGATTAATGTCAGAAACATCTTCTGAGCAAGAAAGATGATGATGATGATGATGATG 3883
DB 4061 AGTGATTAATGTCAGAAACATCTTCTGAGCAAGAAAGATGATGATGATGATGATGATG 4120
QY 3884 AAGGATTAATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 3943
DB 4121 AAGGATTAATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 4180
QY 3944 CGTGTGAGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4003
DB 4181 CGTGTGAGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4240
QY 4004 ATTTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4063
DB 4241 ATTTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4300
QY 4064 TACTCGTGGCTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4123
DB 4301 TACTCGTGGCTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4360
QY 4124 CCAATTTGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4183
DB 4361 CCAATTTGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4420
QY 4184 CCAAGTTGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4243
DB 4421 CCAAGTTGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4480
QY 4244 TTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4303
DB 4481 TTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4540
QY 4304 GGAATTTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4363
DB 4541 GGAATTTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4600
QY 4364 AACACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4423

Db	4601	AACACTCAATCATCTGCGCTTGAATTTTAAGATTGCTAGGCACACTGACCGCTCA	4660
Oy	4424	TCCCTTCACATTTTGTCTCTGTGTTTACGAGATGTGGCTCTTGTTGTTTGAAGTTCAAC	4483
Db	4661	TCCCGTACACACTGTCTCCCGGGGCTCGCGGAGCTGGCCGTGGCTGTAGAACTTCAGC	4720
Oy	4484	CTCAGCAGACACTCCATTCACAAAGAGACTACTGAAAGCATCTGCTTTGTACTACATGT	4543
Db	4721	CTCAGAGACCGGCCCTCCCTCCAGAGAGACTGCTGAACATCCGGTCTTCCGTACACAGTGGT	4780
Oy	4544	AGCCAAATTAATGACAGATCACTACAGTAAGAAACAGATGCTCAACAAGAAAAAACTT	4603
Db	4781	AGTTAAATTTGTTCAGATCAGCTCTTAATGAGACAGATATGCAACCGGAGAGAAAAGA	4840
Oy	4604	G----TGGGGAACACACTTATATTTCTACTGGCCATGATGCCACCTGAACAGTATGAACG	4659
Db	4841	GAACCTTGTGGGCGACCACTGTGCGCTAAACCGAGCCCTCACGCCACCTGAACACCCGAAACG	4900
Oy	4660	AGGCGACTGGGGAAACCCCTTACCTAAGTATGTGATTGACAAATCAAGATCTTACTAAGC	4719
Db	4901	GGGCGACAGGGGAA--CCGTACCTTAACCATGTGATTGACAAATCAAGACTCTTACTAAGC	4959
Oy	4720	TCAATATGCA--AAAGCCAAACTAGTGTGCAAAACGTGTAATCTGTGCTTTCAAGAACTG	4778
Db	4960	TGCGATATGCAAGACACTCTACAGCTCTGTGCAAGAACTGTACACCCGTCCTTTTACAGGACTG	5019
Oy	4779	GCCCTAGGTGACAGGAAACCAATGAAGTTGCGATGACTAAATTCAGAGCATTAATTT	4838
Db	5020	GCTCTGGGGGACCGAAGAGCCATGTGAGTTTGCATGACTTAAGAAACAGAACATTAATTT	5079
Oy	4839	ATTTTTTTGGAGCACCTTTTTCAGCAA 4864	
Db	5080	A--TTTTTGGAGCACCTTTTTCAGACTA 5103	
RESULT 8			
AAZ25069			
ID	AAZ25069	standard; cdna; 3911 BP.	
XX	AAZ25069;		
XX	09-DEC-1999	(first entry)	
XX	Human MEK1 nucleotide sequence.		
XX	MEK1; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK;		
KW	extracellular regulated kinase; signal transduction; regulation;		
KM	MAPK/ERK; MEK; MKRK; inflammation; cellular proliferation;		
XX	differentiation; development; cell death; ss.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	3..3911	
FT		/tag="a	
FT		/product="MEK1"	
XX	W09947686-A2.		
XX	23-SEP-1999.		
XX	15-MAR-1999;	99MO-US05556.	
XX	16-MAR-1998;	98US-0078153.	
PR	04-SEP-1998;	98US-0099165.	
XX	(CADU-) CADUS PHARM CORP.		
XX	Johnson GL;		
XX	WPI; 1999-571843/48.		
XX	P-PSDB; AA42104.		
OR			

XX	New human MEK polynucleotides and polypeptides, used for regulating
PT	signal transduction in cells -
PS	Claim 2; Fig 1; 15pp; English.
XX	The present sequence encodes human mitogen-activated protein kinase/ extracellular response kinase (MAPK/ERK) kinase kinase (MEKK), specifically designated MEKK1. The MEK proteins are used to modulate CC and regulate signal transduction in cells, as well as for regulation of gene transcription in a cell encoding MEKK, where the cell is involved CC in inflammation, regulation of cellular proliferation and differentiation, regulation of development, regulation of cell death or regulation of inflammation. They are also used to prepare antibodies. CC MEK polynucleotides can be used to produce the protein recombinantly and as a source of probes and primers.
SQ	Sequence 3911 BP; 1058 A; 973 C; 975 G; 905 T; 0 other;
Query Match	62.7%; Score 3286.4; DB 20; Length 3911.
Best Local Similarity	90.5%; Pred. No. 0;
Matches 3580;	Conservative 0; Mismatches 331; Indels 45; Gaps
OY	590 CAGCCTGGAAGCAGAAATGGTTGAAAAGAGAATAAGCGAGGCGCTGTGCGTAAAC 649
DB	1 CGCGCTGGAAAGCACAGATGGTTGAAAAGAGAATAAGCGAGGCGCTGTGCTAACC 60
OY	650 CAATCCCAATTAAAGAGATGGATGTGAAATGAATCATTACACTGTGAGTCACAGAG 709
DB	61 CATCCCAATTAAAGAGATGGATGTGAAATGAATCATTACACTGTGAGTCACAGAG 120
OY	710 AGGTCCAGGCAAGTGCGGGTTCACACAGCTTCCAAAGGCCGACGAGTCCTTCCGTGCA 769
DB	121 AGGTCCAGGCAAGTGCGGGTTCACACAGCTTCCAAAGGCCGACGAGTCCTTCCGTGCA 180
OY	770 ACTCCCATCAGAGTGCACACATGAATATCAGATCTCCAGAGTAAGAGAAAAAGATT 829
DB	181 ACTCCCATCAGAGTGCACACATGAATATCAGATCTCCAGAGTAAGAGAAAAAGATT 240
OY	830 CCCGAGTGCTTTTGAAGATGGCAGAAATCACACACCCCAGAGAGCCCCCTTACAGANTG 889
DB	241 CCCGAGTGCTTTTGAAGATGGCAGAAATCACACACCCCAGAGAGCCCCCTTACAGANTG 300
OY	890 GCCTCTACCATATAGCCCTGAGAAACAACCGCGGTGTTAACAAAGTAGTGCAGGCCA 949
DB	301 GCCTCTACCATATAGCCCTGAGAAACAACCGCGGTGTTAACAAAGTAGTGCAGGCCA 360
OY	950 GACCTACTACTATGAGAGCAGATAGGGCCCTAACTCTTCTGATTGGAGAGACACCCAG 1009
DB	361 GACCTACTACTATGAGAGCAGATAGGGCCCTAACTCTTCTGATTGGAGAGACACCCAG 420
OY	1010 ACAATAAATACCGGGTGTTTATGGGCGCTCAGAACTGCAGAGTGCACAGTGAACATTCT 1069
DB	421 ACAATAAATACCGGGTGTTTATGGGCGCTCAGAACTGCAGAGTGCACAGTGAACATTCT 480
OY	1070 GTATTCACTGCTATTGTGATGCTCCGGGTGTTCAACTAGAACCTTCAGACCCAATGT 1129
DB	481 GTATTCACTGCTATTGTGATGCTCCGGGTGTTCAACTAGAACCTTCAGACCCAATGT 540
OY	1130 TTATGGAAAAAAGCTTTAAAGAAATTTTGAAGGTGAGAGTTTGTTCAGAAATATCACAGA 1189
DB	541 TTATGGAAAAAAGCTTTAAAGAAATTTTGAAGGTGAGAGTTTGTTCAGAAATATCACAGA 600
OY	1190 GGCGTAGCTCAAGATCAAAGCTCCATCTCGTAACACCATCCAGAAAGTTTGTTCACGCA 1249
DB	601 GGCGTAGCTCAAGATCAAAGCTCCATCTCGTAACACCATCCAGAAAGTTTGTTCACGCA 660
OY	1250 TGTCAATTTCTATACATTTGTATCTATCTAGTACTTCTAAGCTGTAGTTACAGAAAACAGA 1309
DB	661 TGTCAATTTCTATACATTTGTATCTATCTAGTACTTCTAAGCTGTAGTTACAGAAAACAGA 720
OY	1310 TAAAGATGAAGAGAACAGATGTCTCATTTGCTGTGGGCAATGCTGTATGAAGAA 1369

Db 721 TAAAGATGAAGAGAGAGATGTGTCTATTGCTTGTGGGCAATGCTTGAAGAA 780
Oy 1370 GTCTTACAGTGTGTGAAGAGCGCTGCAGAGAACAGCTGCACCACTGCATGTCAATT 1429
Db 781 GCTTACAGTGTGTGAAGAGCGCTGCAGAGAACAGCTGCACCACTGCATGTCAATT 840
Oy 1430 GGGCAGAGAGTGTGAAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCTAACT 1489
Db 841 GGGCAGAGAGTGTGAAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCTAACT 900
Oy 1490 GAGATCTCATATTTCTACAGCAGAGTGTGCAAGCTCTGTGATGATTCCTTCTCC 1549
Db 901 GAGATCTCATATTTCTACAGCAGAGTGTGCAAGCTCTGTGATGATTCCTTCTCC 960
Oy 1550 TCAGAGCTGCACAGCAGCAACCGTACAGCAGCAGCCTTGTGCTGATCAGAGAAATC 1609
Db 961 TCAGAGCTGCACAGCAGCAACCGTACAGCAGCAGCCTTGTGCTGATCAGAGAAATC 1020
Oy 1610 AAGAGAGCAATTTTAACTTACTCATATGAACTGAACTGCTGTGCTTATTTCTA 1669
Db 1021 AAGAGAGCAATTTTAACTTACTCATATGAACTGAACTGCTGTGCTTATTTCTA 1080
Oy 1670 ATTATGCTGAGCAGTGTAGTGTGCTGTGAAATGGAATGGAATGCTGTGCTTATTTCTA 1729
Db 1081 ATTATGCTGAGCAGTGTAGTGTGCTGTGAAATGGAATGGAATGCTGTGCTTATTTCTA 1140
Oy 1730 GAACTGGAATGTAGAGAGATGCGCCCTCAGCGCTTTCCTCCATGATGATGAGGCGCC 1789
Db 1141 GAACTGGAATGTAGAGAGATGCGCCCTCAGCGCTTTCCTCCATGATGATGAGGCGCC 1200
Oy 1790 TGTCTGTGCAAAATGGGGAGAGCAGCTGGAATTTCTGGGGGAGAGTGGAGAGCCCA 1849
Db 1201 TGTCTGTGCAAAATGGGGAGAGCAGCTGGAATTTCTGGGGGAGAGTGGAGAGCTTAA 1260
Oy 1850 GTGGGAGCCACAGTGTGCTTCCACAGCAGTATCTCAGAGATGATGAGGAGCAT 1909
Db 1261 GTGGGAGCCACAGTGTGCTTCCACAGCAGTATCTCAGAGATGATGAGGAGCAT 1320
Oy 1910 GCTGAGCCTTGTCTCAATGATGCTGTGCTGACCTGTCTCAAAAGTGTAGTGTCTT 1969
Db 1321 GCTGAGCCTTGTCTCAATGATGCTGTGCTGACCTGTCTCAAAAGTGTAGTGTCTT 1380
Oy 1970 TAAAAACATTTGAGAGCAGTGTGATATATCTCTTCCAGAGTTAGGGGAAAGATCA 2029
Db 1381 TAAAAACATTTGAGAGCAGTGTGATATATCTCTTCCAGAGTTAGGGGAAAGATCA 1440
Oy 2030 AACTTCAGAGCTTCTCCAGCAGTGTGATGACACATCTGATCAATGTCAGATGCCA 2089
Db 1441 AACTTCAGAGCTTCTCCAGCAGTGTGATGACACATCTGATCAATGTCAGATGCCA 1500
Oy 2090 ATAGCCGACAAAGTGTCTCATATCAACATGTTGGAATCTGCAAGGCCAAGCAG 2149
Db 1501 ATAGCCGACAAAGTGTCTCATATCAACATGTTGGAATCTGCAAGGCCAAGCAG 1560
Oy 2150 GAGAGTGGCAGTGGCAGAGAAATCTAAAGCTGATTCATTTGATTTGGTGTG 2209
Db 1561 GAGAGTGGCAGTGGCAGAGAAATCTAAAGCTGATTCATTTGATTTGGTGTG 1620
Oy 2210 ATTATGCTTAAATGTTATTTTGAACCAAACTGAATCAAACTTGGCAAGACTTC 2269
Db 1621 ATTATGCTTAAATGTTATTTTGAACCAAACTGAATCAAACTTGGCAAGACTTC 1680
Oy 2270 TTTGGCCGCTTGTCTTATAGATAGACTGTGTGGAATTTCTGCTGAATTTATCTTC 2329
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Oy 2330 ATATTGTCACTGTATGTTTCAAGCTGAGCCTGTGAAATCAGGTATAGAACTGC 2389
Db 1741 ATATTGTCACTGTATGTTTCAAGCTGAGCCTGTGAAATCAGGTATAGAACTGC 1800
Oy 2390 TGTCTGTCTTAACTTGTCTTGTGCACTGATTAATTTCCACTGTAATGTGGCAAC 2449
Db 1801 TGTCTGTCTTAACTTGTCTTGTGCACTGATTAATTTCCACTGTAATGTGGCAAC 1860
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Oy 2510 CAAACGTGTAAGAAATGCTAGTGTTCAGTTCACCTACTCTTACACAGATGCGTCCG 2569
Db 1921 CAAACGTGTAAGAAATGCTAGTGTTCAGTTCACCTACTCTTACACAGATGCGTCCG 1980
Oy 2570 GTTTGATGCTATTTGAGATGAGTGAATGCGCAATTCAGTTCAGTTCAGTTCAGTTCAG 2629
Db 1981 GTTTGATGCTATTTGAGATGAGTGAATGCGCAATTCAGTTCAGTTCAGTTCAGTTCAG 2040
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Oy 2810 CAGTACGACTTCTAGTTCAGACAAACAAACAAACAAACAGAGCAACCAACCA 2869
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Oy 2870 TGTGTTAAACAAAGCAGACACCCACAGTCAAGTGTGAACTCTCTTATCTCATC 2929
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Oy 2930 ATTCCCAATTAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTACCCCATGTGACAG 2989
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Oy 2990 CTGGCAGCTCAACAGATGCTTAAACATAGACTTGAAGGATTCATTCCTGCAAAATAC 3049
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Db 2476 AAAACAAAGATCAGATTAACCTTCCAGTCTTCTCTGATGATGATGATGATGATGATG 2535
Oy 3170 GTAACTATACAGAGCCCAAGCCATCTAGACCTTACCCAGGATATACAGTAAACAGGAG 3229
Db 2536 GTAACTATACAGAGCCCAAGCCATCTAGACCTTACCCAGGATATACAGTAAACAGGAG 2595
Oy 3230 ATCCCTCAAAAAATGACATGACACTGTGATGACAGTGTGATGATGATGATGATGATG 3289
Db 2596 ATCCCTCAAAAAATGACATGACACTGTGATGACAGTGTGATGATGATGATGATGATG 2655
Oy 3290 TTTGGCTGTGACAGATTAAGTAAATGATGATGATGATGATGATGATGATGATGATGATG 3349
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Db 2776 TTTCTTAAAGATTAATGCTTCAAGTGTGATGATGATGATGATGATGATGATGATGATG 2835
Oy 3470 TCTGTCTCTGAAAGGCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 3529
Db 2836 TCTGTCTCTGAAAGGCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 2895

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QY 3530 AAAAGTGCAGAGAGATGCAAGCTGAGAGAGAAAGCTTTACCAATTGGCAGTCAA 3589
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QY 3590 TGTCAAGCTCTCAGAGATCCCTCCCATAGTTCCTCAGCTGAGGTTGAAATGGAGAG 3649
Db 2956 TGTCAAGCTCTCAGAGATCCCTCCCATAGTTCCTCAGCTGAGGTTGAAATGGAGAG 3015
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Db 3796 CACATTTGTCCTGCTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3855
QY 4490 ACAGAGCTCTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4545
Db 3856 ACAGAGCTCTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3911
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RESULT 9
AAx80912
ID
AAx80912 standard; cDNA; 3911 BP.
XX

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AC AAX80912;
XX
DT 03-NOV-1999 (first entry)
XX
DE Human MEK1 cDNA.
XX
KW Human MEK1 cDNA; Mitogen ERK kinase 1 protein; MEK1; protease;
KW extracellular signal regulated kinase; ERK; signal transduction pathway;
KW regulation; apoptosis; protein kinase; cleavage; caspase; antibody;
KW kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection;
KW immunoreactive; diagnostic; therapeutic assay; reagent; disorder;
KW aberrant expression; activation; MEK1 gene product; DNA probe; primer;
KW selectively hybridise; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3..3911
FT FT /*tag= a
FT FT /product= "MEK1 protein"
FT FT /function= "Regulates cellular apoptosis"
FT FT mat_peptide 2052..3908
FT FT /*tag= b
FT FT /note= "Active fragment that mediates apoptosis"
XX
XX W09941385-A1.
XX
PD 19-AUG-1999.
XX
PE 12-FEB-1999; 99WO-US02974.
XX
PR 13-FEB-1998; 98US-0023130.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Johnson GL;
XX
XX WPI; 1999-508649/42.
XX
DR P-PSDB; AAY26235.
XX
XX
PT A new mammalian serine-threonine protein kinase for treating
PT disorder characterized by aberration of the enzyme gene
XX
XX
PS Claim 5a; Page 124-130; 149pp; English.
XX
XX
CC The present sequence is an isolated human MEK1 cDNA. It encodes
CC Mitogen ERK Kinase 1 (MEK1) protein, which functions to
CC integrate proteases and signal transduction pathways involved in the
CC regulation of apoptosis. It is a 196 kDa protein kinase, which upon
CC cleavage at Asp 681/684 by caspase generates a 91 kDa kinase fragment
CC that induces apoptosis and a 113 kDa NH2-terminal fragment. Mutant MEK1
CC proteins that are resistant to cleavage by caspase proteases and capable
CC of inhibiting apoptosis can be produced. MEK1 proteins and antibodies
CC immunoreactive with MEK1 proteins are used in diagnostic and therapeutic
CC assays and reagents for detecting and treating disorders involving
CC aberrant expression or activation of the MEK1 gene products. DNA probes
CC or primers that selectively hybridise to MEK1 cDNA, can be used for its
CC detection in samples.
XX
S0 Sequence 3911 BP; 1058 A; 973 C; 905 T; 0 other;
XX
XX
Query Match 62.7%; Score 3286.4; DB 20; Length 3911;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;
XX
QY 590 CAGCTGGAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 649
Db 1 CGGCTGGAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 650 CAATCCAGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 709
Db 61 CAATCCAGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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QY	710	AGGTCCAGGCAATGTCGGGCTTCA	CACAGCTTCCAAGGCGACGAGCTCTCTCGGCA	769
Db	121	AGGTCCAGGCAATGTCGGGCTTCA	CACAGCTTCCAAGGCGACGAGCTCTCTCGGCA	180
QY	770	ACTGCCATCAGGTCGCGACGTGA	AAATCTCCAGAGTAAGGAGAAAATAGTTT	829
Db	181	ACTGCCATCAGGTCGCGACGTGA	AAATCTCCAGAGTAAGGAGAAAATAGTTT	240
QY	830	CCCCAGTGCCTTTTCAGAGTGG	CAGATCCACACACCCCGAAGAGCCCTTCACAGATG	889
Db	241	CCCCAGTGCCTTTTCAGAGTGG	CAGATCCACACACCCCGAAGAGCCCTTCACAGATG	300
QY	880	GCTTCTCACCATATAGCCCTG	AGAAACAACCGCGGTATACAAATGATGCGGCGCA	949
Db	301	GCTTCTCACCATATAGCCCTG	AGAAACAACCGCGGTATACAAATGATGCGGCGCA	360
QY	950	GAGCTGCTTACATGCGACACAT	ATAGGGCTATACCTTCTGATGTGGAGAGACACCCAG	1009
Db	361	GAGCTGCTTACATGCGACACAT	ATAGGGCTATACCTTCTGATGTGGAGAGACACCCAG	420
QY	1010	ACAAATAAATACCGGGCTTTAT	TATGGGCGCTCAGAACTGCAGCTGCACGTGGAAATCTCT	1069
Db	421	ACAAATAAATACCGGGCTTTAT	TATGGGCGCTCAGAACTGCAGCTGCACGTGGAAATCTCT	480
QY	1070	GTATTCATCTGCTATTTTGTAT	GTGTCGCGGCTTTCACTAGAACCTTCAGACCAATGT	1129
Db	481	GTATTCATCTGCTATTTTGTAT	GTGTCGCGGCTTTCACTAGAACCTTCAGACCAATGT	540
QY	1130	TATGAGAAAAAATCTTTAA	CAATTTTTSAGTTTGGATTTTCCAGAAATATCAGATTA	1188
Db	541	TATGAGAAAAAATCTTTAA	CAATTTTTSAGTTTGGATTTTCCAGAAATATCAGATTA	600
QY	1190	GGCGTACGTCGAAGATCAAG	ATCAAGCTCCTGTATACACATCCAGAAAGTTTGTATACGCA	1249
Db	601	GGCGTACGTCGAAGATCAAG	ATCAAGCTCCTGTATACACATCCAGAAAGTTTGTATACGCA	660
QY	1250	TGTCAAATCTCATCATCTTGT	CATCATATGATCTTCTAGTCTAGTTCCAGAAAACAGCA	1309
Db	661	TGTCAAATCTCATCATCTTGT	CATCATATGATCTTCTAGTCTAGTTCCAGAAAACAGCA	720
QY	1310	TAAAGAGTGAAGAGACACAT	GTGTCTCTATTTGCTTGTGGGCAATGCTTATGAAAGAA	1369
Db	721	TAAAGAGTGAAGAGACACAT	GTGTCTCTATTTGCTTGTGGGCAATGCTTATGAAAGAA	780
QY	1370	GTTCTTACAGTGTGAGAGAG	GCGCTGCAGAGAACAGCTGCACACCACTGCATGTCATATT	1429
Db	781	GTTCTTACAGTGTGAGAGAG	GCGCTGCAGAGAACAGCTGCACACCACTGCATGTCATATT	840
QY	1430	GGGCGAAGAGTGTAGAAGAA	TATAGAAACCTTTAATATGTCCCTTTGTATAGTAAAT	1489
Db	841	GGGCGAAGAGTGTAGAAGAA	TATAGAAACCTTTAATATGTCCCTTTGTATAGTAAAT	900
QY	1490	GGAGATCTCATGATTTTCA	AGCCAGAGTGTCAAGTCTGTGGAATTCCTCTTCTCC	1549
Db	901	GGAGATCTCATGATTTTCA	AGCCAGAGTGTCAAGTCTGTGGAATTCCTCTTCTCC	960
QY	1550	TCAGAGCTGCACAGCAGCA	CAACCGTACAGAGCAGCTTTGGCTGTGATCAGCAAGAAATC	1609
Db	961	TCAGAGCTGCACAGCAGCA	CAACCGTACAGAGCAGCTTTGGCTGTGATCAGCAAGAAATC	1020
QY	1610	AAGAGAGCAATTTTAACTT	ACTCATTTATGGAATCAGCAAAATCCCTCTGTTCAAAAG	1669
Db	1021	AAGAGAGCAATTTTAACTT	ACTCATTTATGGAATCAGCAAAATCCCTCTGTTCAAAAG	1080
QY	1670	ATTATTAAGTCGAGCCAT	TGATTCAGAGTGTGGAAATGGAATCTGTTGGCTCTTATCTTA	1729
Db	1081	ATTATTAAGTCGAGCCAT	TGATTCAGAGTGTGGAAATGGAATCTGTTGGCTCTTATCTTA	1140
QY	1730	GAACACTGGAATGTATAGAG	ATATGAGATGGCCCTCAGAGGCTTTTCCCATATGTCACATGGGCGCC	1789
Db	1141	GAACACTGGAATGTATAGAG	ATATGAGATGGCCCTCAGAGGCTTTTCCCATATGTCACATGGGCGCC	1200
QY	1790	TGCTGTGTGGCAATGGGG	AGAGCATCTGGAATTTCTGGGGGCGACAGTGGAAACAGCCGCA	1849

Db 2254 CGGTTCAAAACAAAGGACAGACCCCAAGTCAGTGTGAACTCTCCCTTTGTC---TC 2310
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 Db 2368 -----CAGATATTTCTAAGCAGACAGCCCGAGCATTTGTTCCCTCGAAGTAC 2415
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 Db 2596 ACGCCACAAAAAGTAGCATGACACTGATCTGGGAGTGTCTTCCAGGTGTAGACAGCT 2655
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 Db 2656 TTGGGCGCGCGGCAACATGTGCAACCGCTCATCCCGACGACGACAGTGTACCC 2715
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 Db 2836 TCCCTGCT 2895
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QY 4010 TGAATTAATGAGACCTTTCAAAAGATCAGTACTATTATTAACACTGACAGCTTACTCC 4069
 Db 3376 TGAATTAATGAGACCTTTCAAAAGATCAGTACTATTATTAACACTGACAGCTTACTCC 3435
 QY 4070 GTGGCTTGTATCTCCATGAAACCAAAATCATTCACAGAGATGATGAAAGGTGCCANT 4129
 Db 3436 GTGGCTTGTATCTCCATGAAACCAAAATCATTCACAGAGATGATGAAAGGTGCCANT 3495
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RESULT 10
 AAQ79325
 ID AAQ79325 standard; cDNA; 3260 BP.
 XX
 AC AAQ79325;
 XX
 DT 28-JUN-1995 (first entry)
 XX
 DE Mammalian MEK kinase (MEK 1) cDNA.
 XX
 KW MEK kinase; MEK 1; mitogen-activated protein kinase regulator;
 KW MAPK; cell atrophy inhibition; Parkinson's; Alzheimer's; cancer;
 KW autoimmune diseases; allergies; wound healing; oncogenes;
 KW tumour agents; neurotropic growth factor; ds.
 XX
 OS Mus musculus.
 XX
 FH key Location/Qualifiers
 FT CDS 486..2504
 FT /*tag= a
 XX
 PD W09424159-A.
 XX
 PD 27-OCT-1994.
 XX
 PF 15-APR-1994; 94WO-US04178.
 XX
 PR 15-APR-1993; 93US-0049254.
 XX
 PA (NALE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 PI Johnson GL;
 XX
 DR WPI: 1994-357747/44.
 DR P-PSDB: AAR66029.

XX New MEK kinase protein and related antibodies and nucleic acid
PT regulator of mitogen activated protein kinase, useful
PT therapeutically to inhibit cell atrophy, to screen for oncogenes
etc.
PS Claim 6; Page 8; 84pp; English.
XX
XX AA079325 encodes AAR6029 the mammalian MEK kinase (MEK 1), other
CC unique mammalian MEK kinases identified by PCR as described in
CC AAR6030 (MEK 2), AAR6031 (MEK 3) and AAR6032 (MEK 4). MEK is an
CC activator, independent of Raf protein, of mitogen-activated protein
CC kinases (MAPK). Inactivation of MEK can be used in the treatment
CC of some cancers, autoimmune diseases and allergies, while
CC stimulation can promote wound healing. MEK can also be used to
CC alleviate cellular atrophy in Parkinson's or Alzheimer's by acting
CC as a neurotrophic growth factor, and to screen for oncogenes and
CC tumour agents.
XX
SQ Sequence 3260 BP; 869 A; 837 C; 793 G; 761 T; 0 other;
Query Match 37.3%; Score 1955.6; DB 15; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;
QY 1996 TATATCTCTTCCACAGTTTACGCGAAGAAATCAAACTTCAGAGACTTTCACGCCAGTT 2055
Db 1 TACACTCTCTTCCACAGTTTACGCGAAGAAATCAAACTTCAGAGACTTTCACGCCAGTT 60
QY 2056 GTAGACACATCTCTTACGAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 2115
Db 61 GTAGACACATCTCTTACGAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 119
QY 2116 TCAACACTGTGTGAAGTGTGCAAGAGCCAAAGCAGAGAGAGTGGCAGTTGGCAGAGAAATA 2175
Db 120 TCAACACTGTGTGAAGTGTGCAAGAGCCAAAGCAGAGAGAGTGGCAGTTGGCAGAGAAATA 179
QY 2176 CTAAAGCTGTGATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2235
Db 180 CTAAAGCTGTGATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 239
QY 2236 AACCAACTGTGATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2295
Db 240 AACCAACTGTGATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 299
QY 2296 CTGTGTGTGAATTTCTGTGTGAATTTCTGTGTGAATTTCTGTGTGAATTTCTGTGTGA 2355
Db 300 CTGTGTGTGAATTTCTGTGTGAATTTCTGTGTGAATTTCTGTGTGAATTTCTGTGTGA 359
QY 2356 GCTGAGCTGTGTAATTCAGATTAAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2415
Db 360 GCTGAGCTGTGTAATTCAGATTAAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 419
QY 2416 TCCATTTATTAATTCAGATTAAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2475
Db 420 TCCATTTATTAATTCAGATTAAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 479
QY 2476 GCAAGAAATGTGTACTAGATACCCCATGTGTTTCAAAACTGTGTAAGAAATGTGTAAG 2535
Db 480 GCGAGAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 539
QY 2536 TCCAGTTTCACTCTTACAGAGATGCGTGGCTTTGATGGCTATTTGACAGATGAGGTG 2595
Db 540 TCCAGTTTCACTCTTACAGAGATGCGTGGCTTTGATGGCTATTTGACAGATGAGGTG 599
QY 2596 GAAATTTCCGAAAGCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2655
Db 600 GAAATTTCCGAAAGCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 658
QY 2656 TTTCTTGAGAGCATCTGTTCACAACTATCTGAGAAACACAGAGAAAGTTCCTCTGAG 2715
Db 659 --CTTACAGAGCGGTGGCCCAACAGCTGTCT-----AGAAACAGAGTTCCTCTGAG 707

QY 2716 TGCACAGTCCATTTAGAGAAATCTGGAAGAGATTAATGCTACAAAATTTAGTCCAGT 2775
Db 708 CACACAGTCCATTTAGAGAAATCTGGAAGAGATTAATGCTACAAAATTTAGTCCAGT 767
QY 2776 TCAAGAGCATTTCTGAGAGCTGGCCAGATTCATTAAGAGCTTCTAGTCAACACA 2835
Db 768 TCGAGAGCATTTCTGAGAGCTGGCCAGATTCATTAAGAGCTTCTAGTCAACACA 819
QY 2836 ACAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2895
Db 820 -----CAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 872
QY 2896 AGTAGAGTTTGAAGCTCTCTCTTATCTCATATTCATTCATTAATTTTCCAGCTTG 2955
Db 873 AGTAGAGTTTGAAGCTCTCTCTTATCTCATATTCATTCATTAATTTTCCAGCTTG 929
QY 2956 TCAACCCCTTCTCTTCTTACCCCATCTGTAACAGTGTGACAGTGTGACAGTGTGACAG 3015
Db 930 TCAACCCCTTCTCTTCTTACCCCATCTGTAACAGTGTGACAGTGTGACAGTGTGACAG 974
QY 3016 CATAGACTTCAGAGATTCATTCCTGCAAGATACCTTCTGATCTCTCAACACAGCGC 3075
Db 975 CACAGACCCCGAGCATTTGTTCCCTGCAAAATACCTTCCGATCTCTCAACACAGCGC 1034
QY 3076 AAGTTTCTCTACAAATTCACAGAAACTGTCTGAAACAAAGCTCAGATTAATTTTCC 3135
Db 1035 AAGTTTCTCTACAAATTCACAGAAACTGTCTGAAACAAAGCTCAGATTAATTTTCC 1094
QY 3136 CCACTTCTTACAGTGTGCAAGCCCTGCGCTGCAATACAGACAGCCCAACAGCTCT 3195
Db 1095 CCACTTCTTACAGTGTGCAAGCCCTGCGCTGCAATACAGACAGCCCAACAGCTCT 1154
QY 3196 AGACCTACCCAGGTAAATACAAAGTAAACAGAGATCCCTCAAAAATAGCATACACT 3255
Db 1155 AGACCTACCCAGGTAAATACAAAGTAAACAGAGATCCCTCAAAAATAGCATACACT 1214
QY 3256 GATCTGAACAGTACATTCCTCAATTTGATGACAGCTTTGGCTGTGACAGCATAGTAT 3315
Db 1215 GATCTGAACAGTACATTCCTCAATTTGATGACAGCTTTGGCTGTGACAGCATAGTAT 1274
QY 3316 GCTGTATACCACTGACAGAGAGTGTGACCCAGTACAGAGAGAGAAATGAGATTTGAT 3375
Db 1275 GCTGTATACCACTGACAGAGAGTGTGACCCAGTACAGAGAGAGAAATGAGATTTGAT 1334
QY 3376 GTCAATACAGAGCTCAACTCCAGTATTTGAGAGCTTCTTGAAGCATATCTCTCAAGT 3435
Db 1335 GTCAATACAGAGCTCAACTCCAGTATTTGAGAGCTTCTTGAAGCATATCTCTCAAGT 1394
QY 3436 GATCAACAGTACATTTTAAGTCAAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 3495
Db 1395 GATCAACAGTACATTTTAAGTCAAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1454
QY 3496 GATGATACCTCAAGAGATGATGATCATTAATCAAAAGTCAAAAGAGAGATGGAAGCT 3555
Db 1455 GATGATACCTCAAGAGATGATGATCATTAATCAAAAGTCAAAAGAGAGATGGAAGCT 1514
QY 3556 GAAGAGAGAGAGCTTTAGCAATTTGAGAGTGTGAGCTGTGAGAGTGTGAGAGTGTGAG 3615
Db 1515 GAAGAGAGAGAGCTTTAGCAATTTGAGAGTGTGAGCTGTGAGAGTGTGAGAGTGTGAG 1574
QY 3616 ATATGTTCTCAGCTGACAGTGTGAAATGAGAGATATCATATTTATTCACAGATACA 3675
Db 1575 ATATGTTCTCAGCTGACAGTGTGAAATGAGAGATATTAATCAATTTATTCACAGATACA 1634
QY 3676 CCAGAGACTTCAGAGCATACCAAGCAACCAAGCAACCAAGCAACCAAGCAACCAAGCA 3735
Db 1635 CCAGAGACTTCAGAGCATACCAAGCAACCAAGCAACCAAGCAACCAAGCAACCAAGCA 1694
QY 3736 CTGAAGGTCACAGATAGAGCTTTGAGCATTTCTCTGTTATTCAGGCTCAAGATGTG 3795
Db 1695 CTGAAGGTCACAGATAGAGCTTTGAGCATTTCTCTGTTATTCAGGCTCAAGATGTG 1754
QY 3796 GGAACCTGGAATTTAATGCTGTTAAACAGTGTGACTTATGTACAGAAACATCTTGTGAG 3855


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Db 1755 GGGACTGGGACTTTAAATGGCTGTGMAACAGGTACGTACGTACGAAACACATCTCCGAG 1914
QY 3856 CAAGAAGAAGTACTAGAACACTAAGAGAGATGAAGATGATGAGCCATCTGAATCAT 3915
Db 1815 CAGGAGAGAGTGTGTGAGAGCTTGAGGAGAAAGATCCGGATGATGGGTGTCACCTCAACCAT 1874
QY 3916 CCAAAATATCTTATGATGTTGGAGCCAGCTGTGAGAAAGCAATTAACAATCTCTTCATT 3975
Db 1875 CCAAAATATCTTATGATGTTGGAGCCAGCTGTGAGAAAGCAATTAACAATCTCTTCATT 1934
QY 3976 GAATGATGGCAGGAGATCGGTGCTCATTTGTGAGTAATATGAGAGCTTCAAGAA 4035
Db 1935 GATGATGATGGCAGGAGATCGGTGCTCATTTGTGAGTAATATGAGAGCTTCAAGAG 1994
QY 4036 TCAGTATGATTAATTAACATACATGAAAGTAACTCCGTGGCTTGTATCTCATGAAAC 4095
Db 1995 TCAGTATGATTAATTAACATACATGAAAGTAACTCCGTGGCTTGTATCTCATGAAAC 2054
QY 4096 CAAATATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTGACAGCAGCTGTGAGAG 4155
Db 2055 CAGATATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTGACAGCAGCTGTGAGAG 2114
QY 4156 CTAGAATTCAGATTTTGGAGCTGAGCCAGGTTGGCATCAAAAGAACTGGTGAGGA 4215
Db 2115 CTAGAATTCAGATTTTGGAGCTGAGCCAGGTTGGCATCAAAAGAACTGGTGAGGA 2174
QY 4216 GAGTTTCAGGAGCAATTAATGAGGACAAATTCATTAATGAGCAGTACTAGAGGT 4275
Db 2175 GAGTTTCAGGAGCAATTAATGAGGACAAATTCATTAATGAGCAGTACTAGAGGT 2234
QY 4276 CACACATATGAGAGAGAGCTGTGATGATGAGAGTGTGGCTGTCTTTATGAATGGCT 4335
Db 2235 CACACATATGAGAGAGAGCTGTGATGATGAGAGTGTGGCTGTCTTTATGAATGGCT 2294
QY 4336 TGTGCAAAACACACATGAGATGAGAAAAACACTCCATCATCTTGTGATTAATTAAG 4395
Db 2295 TGTGCAAAACACACATGAGATGAGAAAAACACTCCATCATCTTGTGATTAATTAAG 2354
QY 4396 ATTTGATGATGCAATCTGCTCCATGATCCCTTACATTTGTCCTGTTTACAGAGAT 4455
Db 2355 ATTTGATGATGCAATCTGCTCCATGATCCCTTACATTTGTCCTGTTTACAGAGAT 2414
QY 4456 GTGGCTCTTCGTTGTTTAAACCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4515
Db 2415 GTGGCTCTTCGTTGTTTAAACCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2474
QY 4516 AAGCATCCAGTCTTTCGTACTACATGATGATGATGATGATGATGATGATGATGATGAT 4575
Db 2475 AAGCATCCAGTCTTTCGTACTACATGATGATGATGATGATGATGATGATGATGATGAT 2534
QY 4576 AGGATGCTCAACAGAGAAAAAACTTG---TGGGGAACCATTTGATTTTCTACTGG 4631
Db 2535 AGGATGCTCAACAGAGAAAAAACTTG---TGGGGAACCATTTGATTTTCTACTGG 2594
QY 4632 CCATGATGCTGAGAACACTATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4691
Db 2595 CCATGATGCTGAGAACACTATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2653
QY 4692 ATTGACAAATCATGATCTTACTTACATGATGATGATGATGATGATGATGATGATGATG 4750
Db 2654 ATTGACAAATCATGATCTTACTTACATGATGATGATGATGATGATGATGATGATGATG 2713
QY 4751 ACTGTAACCTGTCCTTTTCAAGAACTGGCTTGGTGAAGAGAGAGAGAGAGAGAGAG 4810
Db 2714 ACTGCAACCGTGTCTTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2773
QY 4811 CATGACTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4864
Db 2774 CATGACTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2825

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RESULT 11

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AAV22676
ID AAV22676 standard; cDNA; 3260 BP.
XX
AC AAV22676;
XX
DT 17-JUL-1998 (first entry)
XX
DE cDNA encoding a murine mitogen-activated protein kinase kinase (MAPKK).
XX
KW Mitogen-activated protein kinase kinase; MAPKK; mouse;
KW extracellular signal-regulated kinase kinase; MEKK; regulation;
KW signal transduction; raf-independent arm; screening assay; treatment;
KW disorder; cancer; autoimmune disease; inflammation; allergy;
KW neuronal disease; Parkinson's disease; Alzheimer's disease; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..485
FT CDS /*tag= a
FT 3'UTR 486..2504 /*tag= b
FT 2502..3260
FT /*tag= c
XX
PN US5753446-A.
XX
PD 19-MAY-1998.
XX
PF 06-JUN-1995; 9505-0472934.
XX
PR 15-APR-1993; 9305-0049254.
PR 14-OCT-1994; 9405-0323460.
PR 21-FEB-1995; 9505-0354516.
PR 12-MAY-1995; 9505-0440421.
XX
PA (MABE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Johnson GL;
XX
DR MPI; 1998-311395/27.
DR P-PSDB; AAM56157.
XX
PT Screening assay for regulators of MEKK signal transduction - using
XX mammalian MEKK polypeptide
XX
PS Claim 6; Columns 29-34; 48pp; English.
XX
CC The present sequence encodes a murine mitogen-activated protein kinase
CC kinase (MAPKK) (also known as extracellular signal-regulated kinase
CC kinase (MEKK)). The protein, which is serine/threonine kinase is capable
CC of regulating signal transduction in cells. It regulates the activity of
CC elements of the raf-independent arm of MEKK. A screening assay for
CC compounds that regulate signal transduction by a MEKK protein complex
CC contacting a reaction mixture containing a mammalian MEKK polypeptide and
CC a test compound and determining the effect of the test compound on an
CC indicator of signal transduction by the MEKK polypeptide in the reaction
CC mixture. Compounds identified by the above assay can be used to prepare
CC therapeutic compositions for treating disorders that are subject to
CC regulation or cure by manipulating a signal transduction pathway in
CC cells involved in the disorders, e.g. cancer, autoimmune diseases,
CC inflammations, allergies, and neuronal diseases such as Parkinson's
CC disease and Alzheimer's disease.
XX
SO Sequence 3260 BP; 869 A; 837 C; 793 G; 761 T; 0 other.
XX
Query Match 37.3%; Score 1955.6; DB 19; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;
QY 1996 TATACCTCTTGGCAGAGTTAGCGGAAGATCAAACTTCACAGAGCTTCCAGCCAGTT 2055
Db 1 TACACTCTTGGCAGAGTTAGCGGAAGATCAAACTTCACAGAGCTTCCAGCCAGTT 60

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[illegible]

OY	3136	CCAACTCTTACTAGTCTAAABACCCCTTGCCCTCCAGTAAATATACAGAGCCAAAGCACTCT	3139
Db	1095	CCAGCTCTTCACTAGTCTAAABACCCCAACCCCTCCAGTAAATATACAGAGCCAAAGCACTCC	1154
OY	3196	AGACCTCTACCCAGGTATATACAAGTAAACAGGAGATACCTCCAAAAAATATAGCATGACATCT	3255
Db	1155	CGACCCGTTCCGGGCACTACAAAGCAAACTATGGGGACGCCCAAAAAAGTATGCTGACATCT	1214
OY	3256	GATCTGAACAGTACTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCACTAGTAGTAAAT	3315
Db	1215	GATCTGGGCAAGTGGTCTTCAGAGTGTGAAGACAGCTTTGGGGGGGGCCCAACGATGGCAAC	1274
OY	3316	GCTGTATTACCCAGTATACAGACAGTGTTCACCCCACTGTAGAGAGAAATGACAGATTAGAT	3375
Db	1275	GCCGTCTATCCACCGACGAGACAGTGTTCACCCCGGTGGAGACAAAGTGCAGGTTTAAAT	1334
OY	3376	GTCAAATACAGGCTCAACCTCAGATATTGAGGACCTTTCTGAAGCACTATATGCTTCAGCT	3435
Db	1335	GTCAGACACCGAGCTCAACTCCAGATCTGAGAGACCTTCTTGAAGCACTTCAGCTTCAGAT	1394
OY	3436	GATACCAACAGTAACTTTTAAATGATCAGAAAGTGTGCTGTCTGTCTCCTGAAGAGGCTGAAAT	3495
Db	1395	GACACGACAGTCACTTTCAAGTCCGAAGTGGCCGTCTCTCTCCGAAAAAGGCCCAAAAT	1454
OY	3496	GATGATTACTTCAAAAGATGATGTGATCATATATCAAAAGTGCNAAGAGAGATGAGACT	3555
Db	1455	GACACACACTTCAAAAGACGACGTCAATCATATTAACAAAGTGCNAAGAAAGATGAGACT	1514
OY	3556	GAAAGAGAAAGAGCTTTAGGAATTTGCCATGGCAATGCCGTCCAGATATCCCTCCCTCC	3615
Db	1515	GAAAGAGAGAGGCTTTAGGAGTATGCCATGGCAATGCCGTCTCAGATATCCCTCCCTCC	1574
OY	3616	ATAGTTCCTCAGCTGCAGGTTTGAAGAAATGAGAAAGATATCATATTATTCACAGATATCA	3675
Db	1575	ATGCTGCTCAGCTGCAGGTTTGAAGAAATGAGAAAGATATATCATATTATCAGAGACACA	1634
OY	3676	CCAGAGACTCTACAGAGACATACCAAAGCAAAACAACGTTATGAGAGAGACACTGATAGG	3735
Db	1635	CCAAACAACTCTTCCAGAGACATACCAAAGCAAAACAACGTTACAGAGAAACGCTGATGG	1694
OY	3736	CTGAAGAGTCAACGATAGAGGCTTTGGAGCACTTTTCCTTGTATACAGGCTCAABATGTG	3795
Db	1695	CTGAAGAGGCTGCAGATAGAGGCTCTGGAGCACTTTTCCTGTTACCAACACAGAGATGTG	1754
OY	3796	GGAATGGAACTTTAATGGCTGTTTAAACAGAGTACTTATGTAGAAACACATCTCTAG	3855
Db	1755	GGGACTGGGAATTTAATGGCTGTGTAAACAGGTACTACTGAGAAACACATCTCTCCAG	1814
OY	3856	CAAGAAGAAGTATGAGAGCACTTAAGAGAAAGATTAAGATATGAGCCATCTGATCAT	3915
Db	1815	CAGAGGAGGTGTGGAAAGGCTTTAGAGGAAGATATCCGATGTGGCTCACTCAACCAT	1874
OY	3916	CCAAACATCATTTAGATCTTTGGAGCCACGTTGTGAAGAAAGCAATTACATCTCTTCAT	3975
Db	1875	CCAAACATCATTCGAGATGCTGGGGGCCACGCTGTGAAGAAAGCAACTCACTCTTCAT	1934
OY	3976	GAAATGGATGGCAGGGATGCGTGGGCTCATTTTCTGATGAATTAATGAGAGCTTTCAAGAA	4035
Db	1935	GAGTGGATGGCGGAGAGATCTGTGTGCTCACTCTTATGATTAATACGAGACTTTCAAGGAG	1994
OY	4036	TCAGTAGTTATTAATCACTACTGAAACAGATTACTCCGTGGCCCTTCGTATCTCCATGAAAC	4095
Db	1995	TCAGTGCATTAATCACTACAGTGAGCAAGTTACTCGTGGGCCCTTCGTATCTCCAGAGAAC	2054
OY	4096	CAAATCATTTACAGAGATGTCCAAAGGTGCCAAATTTGCTAATTGACAGCACTGTGTAGAGA	4155
Db	2055	CAGATCATTTCAAGAGACGTCCAAAGGTGCCAAACCTCTATTTGACAGCACTGTGTAGAGG	2114
OY	4156	CTAAGAATTCAGATTTTGGAGGTGCAAGCCAGGTTGGCATCAAAAGGAACCTGTGACAGA	4215
Db	2115	CTGGAATTTGCAGCTTTGGAGGTGCTGCCAGGTTGGCATCAAAAGGAACCTGTGACAGA	2174
OY	4216	GAGTTTACGGGCAATTAATCTGGGGACAAATGTGATTTATGTGGCACTGTAGGTATTAAGAGGT	4275

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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 2175 GAGTTCACGAGGACAGTACTGGGAGCAATTGCAATTATCATGGCCGCTGAGGTCTTAAGAGGT 2234
Oy 4276 CAACAGTATGGAAGAGAGTGTATGTATGAGATGTGGCTGTCTATTTAGAAATGAGCT 4335
Db 2235 CAGCAGTATGTAGAGAGCTGTATGTATGAGAGTGTGGCTGTATTTAGAAATGAGGT 2294
Oy 4336 TGTGCAAAAACCACTGAGTAATGACAAAAAACAACCTCAATCATCTGCTTTGATATTAAAG 4395
Db 2295 TGTGCAAAAACCACTGAGTAATGACAAAAAACAACCTCAATCATCTGCTTTGATATTAAAG 2354
Oy 4396 ATTGCTAGTGAACACTGCTCATGCTCCCTTCACATTTGCTGCTGTAGAGAT 4455
Db 2355 ATTGCTAGTGAACACTGCTCATGCTCCCTTCACATTTGCTGCTGTAGAGAT 2414
Oy 4456 GTGGCTCTTGTGTTTGTAGACTTCAACCTCAGAGACAGCTCCATCAAGAGACTGCTG 4515
Db 2415 GTGGCTCTTGTGTTTGTAGACTTCAACCTCAGAGACAGCTCCCTCCAGAGAGAGCTGCTG 2474
Oy 4516 AAGCATCCAGTCTTGTGCTACTAGTGTAGCCAAATTATGACATCACTACAGTGAAGAC 4575
Db 2475 AAGCATCCAGTCTTGTGCTACTAGTGTAGCCAAATTATGATCATCTATGAGAGAC 2534
Oy 4576 AGCATGCTCAACAGAGAAAAAAACCTTG---TGGGGAACCAACATGTATTTCTACTG 4631
Db 2535 AGCATGCTCAACAGCGGAGAGAGAAAAAGAACTGTGGGCGACATGCGGCTAACCGCAG 2594
Oy 4632 CCATGATGCTCAACAGCTATGAAAGAGGCGAGGCGAAACCTTACTAGTATGTG 4691
Db 2595 CCTCATCCGCTGAAACAGCAGAAACGCGGCGAGGCGAAACCTTACTAGTATGTG 2653
Oy 4692 ATTGCAATATCATGTATCTGTACTTAAAGCTCAGTATGCA-AAAAGCCAAACTAGTGAAGA 4750
Db 2654 ATTGCAATATCATGTATCTGTACTTAAAGCTCAGTATGCAACATCTACAGCTGTGCAAGA 2713
Oy 4751 ACTGTAACCTGTGCTTCAAGAACTGCGCTAGGTGAACAGAGAAACATGAAGTTTG 4810
Db 2714 ACTGTAACCTGTGCTTCAAGAACTGCGCTAGGTGAACAGAGAAACATGAAGTTTG 2773
Oy 4811 CATGACTAAATTTGCAAGACATTAATTTATTTTGTGAGCACTTTTGAGCAA 4864
Db 2774 CATGACTAAATTTGCAAGACATTAATTTA--TTTTTGTGAGCACTTTTGAGCAA 2825

RESULT 12
AAZ31877 standard; cDNA; 3260 BP.
XX AAZ31877;
AC
XX
XX 24-JAN-2000 (first entry)
DT
XX
DE Mitogen ERK kinase kinase, MEKK-1, coding sequence.
XX
XX Mitogen ERK kinase kinase; MEKK; MEKK-1; neurological disorder; cancer;
KW extracellular signal-regulated kinase; inflammation; autoimmune disease;
KW allergic reaction; hormone related disease; therapy; ds.
XX
XX Mus sp.
OS
XX
XX US5981265-A.
PN
XX
XX 09-NOV-1999.
PD
XX
XX 05-JUN-1995; 95US-0461146.
PF
XX
XX 15-APR-1993; 93US-0049254.
PR 12-MAY-1995; 95US-0440421.
PR 15-APR-1994; 94US-0504178.
PR 14-OCT-1994; 94US-0323460.
PR 14-OCT-1994; 94US-0323460.
PR 14-OCT-1994; 94US-0323460.
PR 14-OCT-1994; 94US-0323460.
PR 28-NOV-1994; 94US-0345516.
XX
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PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
XX Johnson GL;
XX
XX WPI: 1999-633328/54.
DR P-PSDB; AA43318.
XX
XX Regulating mitogen extracellular signal-regulated kinase protein
PT activity, for the treatment of cancer, neurological diseases and
PT autoimmune diseases
XX
XX
XX Claim 1; Column 49-54; 94pp; English.
XX
XX This sequence encodes the mitogen ERK (extracellular signal-regulated
CC kinase) kinase kinase-1 (MEKK-1). The invention relates to a method of
CC regulating MEKK protein activity in a fungal cell by transforming or
CC transfecting the cell with a nucleic acid encoding an MEKK protein. The
CC MEKK protein is useful for treating cancer, inflammation, neurological
CC disorders, autoimmune diseases, allergic reactions, and hormone related
CC diseases.
XX
XX
SQ Sequence 3260 BP; 869 A; 837 C; 793 G; 761 T; 0 other;

Query Match 37.3%; Score 1955.6; DB 20; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

Oy 1996 TATACTCTTTCAGTACAGTTTACGGAAGAAATCAAACTTCAAGACTTCTCCAGCAGTT 2055
Db 1 TACACTCTTTCAGTACAGTTTACGGAAGAAATCAAACTTCAAGACTTCTCCAGCAGTT 60
Oy 2056 GTAGACACCATCTTGTATGTAATGTGCAATAGCCGCAAGATCAGTGTCCATA 2115
Db 61 GTAGACACCATCTTGTATGTAATGTGCAATAGCCGCAAGATCAGTGTCCATA 119
Oy 2116 TCAACACTGTGGAAGTGTGCAAGGCGCAAGGAGAGTGTGGAGTGGCAAGAAATA 2175
Db 120 TCAACACTGTGGAAGTGTGCAAGGCGCAAGGAGAGTGTGGAGTGGCAAGAAATA 179
Oy 2176 CTAAAGCTGTATGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTA 2235
Db 180 CTAAAGCTGTATGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTA 239
Oy 2236 AACCAACTGTAATCAAACTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTA 2295
Db 240 AACCAACTGTAATCAAACTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTA 299
Oy 2296 CTGTGTGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTG 2355
Db 300 CTGTGTGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTG 359
Oy 2356 GCTGAGCTGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTG 2415
Db 360 GCTGAGCTGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTG 419
Oy 2416 TCCATTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTA 2475
Db 420 TCCATTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTA 479
Oy 2476 GCAAGATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTG 2535
Db 480 GCAAGATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTGTAATGTG 539
Oy 2536 TCCAGTTCCACTCACTTCAACAGATGCGTCCGCTTGTGATGCTATTGACAGATGAGTG 2595
Db 540 TCCAGTTCCACTCACTTCAACAGATGCGTCCGCTTGTGATGCTATTGACAGATGAGTG 599
Oy 2596 GAAATTTGCCGAAGCATCCAGTGTGGCGGTAGAGACACTTTGGATGTCAACAGACAGC 2655
Db 600 GAAATTTGCCGAAGCATCCAGTGTGGCGGTAGAGACACTTTGGATGTCAACAGACAG- 658
Oy 2656 TTTCTGCAAGGCTGTGTTTCCCAACACTATGGAACACAGACAGACAGTTCCTCCCTGAG 2715
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Db	1155	CGACCCGCTCGGGCAGGTACACAGCAAACTAAGGGAGCGCCAAAAAGTAGATGACACTT	1214
Oy	3236	GATGTGAACAGTACTTCCAAATGTATGACAGCTTGGCTGTAGACGACATAGTAGTAAT	3315
Db	1215	GATCTGGGAGGTGCTTCCAGAGGTGTGACGACAGCTTGGCGGGCGGCAACAGTGTGCANC	1274
Oy	3316	GCTCTTTACCACAGTGCAGACAGTAGTTCACCCAGTAGAGACAAATGCAAGATTAAAT	3375
Db	1275	GCCCTCATCCACCGACGAGACAGTGTTCACGCCGCTGGAGACAAAGTCAGGTTAAAT	1334
Oy	3376	GTCATATCAGAGCTCACTCCAGTATTGAGAGACTCTTGAAGCACTATGCTCCAGT	3435
Db	1335	GTGAACACCGAGCTCAACTCCAGCATCGAGAGCTCTTGAAAGCATCCATGCTTCAAGT	1394
Oy	3436	GATACCAACAGTAACCTTTTAAGTGAGAAAGTTGCTGTCTCTCTGAAAAAGGCTGAAAT	3495
Db	1395	GACACGACAGTCACTTCAAGTCCGAAGTCCGCTCTCTCCGGAATAAGCCGAAAT	1454
Oy	3496	GATATATACCTACAAAGATGATGTGAATCATTAATCAAAAGTCGAAAGAGATGAGAGCT	3555
Db	1455	GACACACCTACAAAGACGACGTCAATCATTAACAAAGATGCAAGAAAGAAAGATGAGAGCT	1514
Oy	3556	GAAAGAAAGAGAGCTTTAGCAATTTGCATGCGCAATGTGCGCTCAGAGATGCCCTCCC	3615
Db	1515	GAAAGAGAGAGGCTTTTAGGATCGCATGCGCATGCGCTCAGGATGCTCCCTCCC	1574
Oy	3616	ATATCTTCTCAGCTGCAGTGTGAAATGAGAAAGATATCATATTATCAACAGATACAA	3675
Db	1575	ATGCTCCCTCAGGTGCAGGTGGAAATGGAGAAAGATATATATCATTCATTCAGAGACACA	1634
Oy	3676	CCAGAGACTCTACAGAGACATACCAAGCAAAACAACGATATAGAGAAAGACATGAAATGG	3735
Db	1635	CCAAAGAACTCTTCAGAGACATACCAAGGAAACAGCCTTCACAGAAAGACGCTGAGTGG	1694
Oy	3736	CTGAAAGCTAACAGAGAGGCTTGGAGATTTCTCTGTATACAGGCTCAAGATGTG	3795
Db	1695	CTGAAAGGCCAGCGAGATAGGCTTCGGAGATTTCTCTGTATACCAAGCACAGAGATGTG	1754
Oy	3796	GGAATCGAACTTTAATGGCTGTTTAAACAGGTGACTTATGTACAGAAACAATCTTCTAG	3855
Db	1755	GGGACTGGGACTTTAATGGCTGTGAAACAGGTGAGCTACGTGAAACACATCCCTCGAG	1814
Oy	3856	CAGAAGAAAGTAGTAGACACTTAGAGAGAAAGATATAGAAATGATGAGCCATCTGATCAT	3915
Db	1815	CAGAGAGAGGTGGGAGAGGCTTGAGGAAAGAGATCCGATATGGTGCACCTCAACCAT	1874
Oy	3916	CCAAACATCTTAGAGATGTGGGAGGACAGCTGTGAGAAAGAAATTTACAAATCTTCAATT	3975
Db	1875	CCAAACATCTCCGAGATGTGGGGGACAGCTGTGAGAAAGAAAGCACTCAACCTTCAATT	1934
Oy	3976	GAAATGTGGCAGGGGAGATGGTGGCTCATATTGCTAGTAATATGAGACCCTTCAAAACA	4035
Db	1935	GAGTGGATGGCGGGAGAGATGTGTGGCTCACTCTTAGTAATATACGAGCTTTCAAGAG	1994
Oy	4036	TCAGTAGTATTAACTACACTGACAGTAACCTCCGTGGCTTGGTATCTCCATGAAAC	4095
Db	1995	TCAGTCCCTAATTAACCTACACTGTAGACAGTTAATCGCGGCTTCTCATCTCCAGAGAAC	2054
Oy	4096	CAATTCATTACAGAGATGTCAAAAGTGGCCAAATTGCTAATTGACAGCACTGTGTAGAGA	4155
Db	2055	CAGATCAATTACAGAGACGTCAAAAGGTGCAACCTGTCTATTGACAGACCGGTGAGGG	2114
Oy	4156	CTAAGATTTCCAAATTTTGGAGCTGTGAGCAGAGTTGGACTCAAAAGGAACGTGTGCACAGA	4215
Db	2115	CTGAGAAATTCGACAGCTTTGGAGCTGTGTCCAGGTGTGCAATCAAAAGGAACCGGTGTACAGA	2174
Oy	4216	GAGTTTCAGGAGCAATTAAGTGGGACAAATTCGATTTATGTGCACTGAGGTACTAAGAGT	4275
Db	2175	GAGTTTCAGGAGCAAGTTACTGTGGGACAAATTTGCAATTCATGTGGCGCTGAGGTCTTAAGAGT	2234
Oy	4276	CACAAGTATGGAAGAGCTGTATGTATGTGAGTGTGGCTGTGCTAATTATAGAAATGGCT	4335
	11		11

Db	2235	CAGCAGTATGCTAGAGACCTGTGATGTATGAGAGGTTGGCTGGCCATTTTAATAATGGCT	2299
QY	4336	TGTGCAAAAACCCATGTAATGCAGAAAAACATCCATATCTGCTTTGATTAATTAAG	4395
Db	2295	TGTGCAAAAACCCATGTAATGCAGAAAAACATCCATATCTGCTTTGATTAATTAAG	2354
QY	4396	ATTGCTATGTGAACATCTGCTCCATGCATTCCTCTCAGATTGTGTCTCTGGTTTACGAAT	4455
Db	2355	ATTGCTATGTGAACATCTGCTCCATGCATTCCTCTCAGATTGTGTCTCTGGTTTACGAAT	2414
QY	4456	GTGGCTCTTCGTTTGTATTAAGAACTTCAACCTCAGAGACAGACCTCCATCAACAGAGCTACAG	4515
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QY	4516	AAGCATCCAGTCTCTTCCTACTAGATGGTAGCCATTATGCAGATCAACTACAGTAGAGAAC	4575
Db	2475	AAACATCGCGTCTTCCTAGACAGTGGTATTAATTTGTTCAAGTACAGCTCTAATGGAGAC	2534
QY	4576	AGGATGCTCAACAGAGAAAAAACTTG---TGGGAAACACATGTGATTTCTACTGG	4633
Db	2535	AGGATATCGAAACCGGAGAGAGAAAAGAACTTGTGGGCGACATGCGGCTAACCGGAG	2594
QY	4632	CCATGATGGCCCATCAACAGTATGAACAGACGACGAGGGGGAACCTTTACTTAATGATGTG	4691
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QY	4692	ATTGACAATATCATCTGATCTGACTAAGCTCAGATGCA--AAAGCCAACTAGTGCAGAA	4750
Db	2654	ATTGACAATATCATCTGATCTGACTAAGCTCAGATGCA--AAAGCCAACTAGTGCAGAA	2713
QY	4751	ACTGTAAACTGTGCTTTCAAAGAACTGGCCCTAGGTGAACAGAGAAAACAAATGAATTGG	4810
Db	2714	ACTGCACACCGTGCCTTTACAGAGACGTGCTGGGGGACACAGAGGGGATGGAGTTTG	2773
QY	4811	CATGACTAAATTTGAGAGACGATTAATTTATTTTGGAGCACTTTTACGAA	4864
Db	2774	CATGACTAAAGAACAGAGCATAAATTTTA--TTTTTGGAGCACTTTTTCAGCTA	2825
RESULT 14			
AAAA9222			
ID	AAA49222 standard; cDNA; 3260 BP.		
XX			
AC	AAA49222;		
XX			
DT	19-DEC-2000 (first entry)		
XX			
DE	Murine MEK1 coding sequence.		
XX			
KW	Mouse; MEK1; mitogen ERK kinase kinase; signal transduction pathway;		
KW	apoptosis; cancer; autoimmune disease; inflammatory response;		
KW	allergic response; neuronal disorder; Parkinson's disease;		
KW	Alzheimer's disease; ss.		
XX			
OS	Mus sp.		
XX			
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FT	5'UTR	1..485	
FT		/*tag= a	
FT	CDS	486..2504	
FT		/*tag= b	
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FT		/*tag= c	
XX			
PN	US6074861-A.		
XX			
PD	13-JUN-2000.		
XX			
PE	05-JUN-1995; 95US-0461145.		
XX			
PR	15-APR-1993; 93US-0049254.		
PR	12-MAY-1995; 95US-0440421.		

QY	3676	CCAGAGCTCTACAGAGACATACCAGAAAGCAACACCGCTATAGAGAGACACTGAAATGG	3735
Db	1635	CCAGAAACTCTTCAGAGACACTTACCAAGGGAACAGCCCTACAGAGAAAGCGCTGAGGG	1694
QY	3736	CTGAAAGAGTCAGAGATAGAGCTCTGGAGCATTTCTCTCTGTTATACAGCTCAAGATGTG	3795
Db	1695	CTGAAAGGCCAGAGATAGAGCCCTCGGAGCATTTTCTCTCTGTTACCAGACAGAGATGTG	1754
QY	3796	GGAATCGAACTTTAATGCGTGTAAACAGGTGACTTATGTGAGAAACACATCTTCTGAG	3855
Db	1755	GGGACTGGGACTTTAATGCGTGTAAACAGGTGACTAGCTAGAAACACATCCTCCGAG	1814
QY	3856	CAGAAAGAAATAGTAAGAGACACTAAGAGAAAGATPAAGATATATAGCCATCTGAATATG	3915
Db	1815	CAGAGAGAGGTGGTGGAAAGGTTTGAAGGAAAGATCCGGATATGGGTACCTCAACCAT	1874
QY	3916	CCAAACATCTATTAGATGTGGGAGCCAGCTGTGAGAAAGAGAAATTAACATCTCTCAAT	3975
Db	1875	CCAAACATCTATCCGGATGCTGGGGGCCACAGCTGCGAAGAAAGCACTACAACTCTTCAAT	1934
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Db	1935	GAGTGGATGGCGGAGAGATCTGTGGCTCAACCTTGTAATATACGAGCTTCAAGAG	1994
QY	4036	TCGACTATTATTAACTACACTGAACAGTTACTCCGTGGCCTTTCGTATCTCCAGAAAC	4095
Db	1995	TCGACTCCTATTAACTACACTGAGCAGTTACTGCGTGGCCTTTCCTACTCCACAGAAC	2054
QY	4096	CAAAATCTACAGAGATGTCAAAAGGTGCAATTTGCTAATTGACAGCACTGTGTAGGA	4155
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QY	4156	CTAAGATTTGCAGATTTTGGAGCTGTGACGACAGTTGGCATCAAAAGAACTGTGTACAGA	4215
Db	2115	CTGAGATTCAGACTTTGGAGCTGTGCGCAGGTGGCATCAAAAGAAACGGGTGTACAGA	2174
QY	4216	GAGTTTACGGACAACTTACTGGGGACAATTTATGCGACCTGTAGGTACTAAGAGCT	4275
Db	2175	GAGTTTACGGAGGACGTTACTGGGGACAATTTGCAATTCATGGCCCTGTAGGTCTTAAGAGCT	2234
QY	4276	CAACAGTATGGAAGGACCTGTGATGTATGAGAGTGGGTGTGCTAATATATGAAATGGCT	4335
Db	2235	CAGCAGTATGTAAGGACCTGTGATGTATGAGAGTGGGTGTGCGCAATTAATGAAATGGCT	2294
QY	4336	TGTGCAAAACACCACATGGAATGCGAGAAAAACACTCCAACTCATCTTGCTTGTATTTAAG	4395
Db	2295	TGTGCAAAACACCCTTGGAATGCGAGAAAAACACTCCAACTCATCTTGCTTGTATTTAAG	2354
QY	4396	ATTGCTATGTGCACACTACTGCTCATCATGATCCCTTCACATTTGTCTGTGTTCAGCAT	4455
Db	2355	ATTGCTATGTGCACACTACTGCGACCTCATTCCTGCTCACACTCTCCCGGGTGTGCGGCAC	2414
QY	4456	GTTGGCTCTTGTTGTTTAAAGACTTCAACCTCAGAGACAGACCTCCATCAAGAGAGCTACTG	4515
Db	2415	GTTGGCTCTTGCTGTTTAAAGACTTCAACCTCAGAGACAGACCTCCCTCCCTCAGAGAGCTGCTG	2474
QY	4516	AAGCATCTCACTTTCGTACTACATGATGATGACCAATTTATCTCAGATCAACTACAGTGAAGC	4575
Db	2475	AAACATCTCGGCTTCCGTACACAGTGTGATTAATTTGTTCAATCAAGCTCTATATGGAAGC	2534
QY	4576	AGATGTCTCAACAGAGAAAAAACTTG---TGGGGAACACATGTGATTTCTTACTGG	4631
Db	2535	AGGATATTCGAACCGGGAGAGAGAAAAAGAAACTTGTGGGCGACCATCGCGGTAAACCGAG	2594
QY	4632	CCATGATGCCACTGAAACAGTATGAACAGAGCCAGTGGGGAACCTTACTTAAGTATGTG	4691
Db	2595	CCGTCACGCCACTGAAAGAGCAAAACAGGGGGCCAGCGGGGAA--CCGTACCTAAGCATGTG	2653
QY	4692	ATTGACAAATCATGATCTGTACTTAAGCTACAGTATGCA--AAAGCCAAACATGTGTCAGAA	4750
Db	2654	ATTGACAAATCATATGACTGTACTTAAGCTGTGATGTGCAACACTCTACAGCTGTGTGACAGA	2713
QY	4751	ACTGTAACTGTGCTTTTCAAGAACTGTGCCCTTGTAGTGAACAGAAAAACATGAATGTTTG	4810

DB	2714	ACTGACACGCGTCCCTTTCACAGAGACTGCGCTCTGGGGGACACAGAGCCATGTGAGTTTG	2773
OY	4811	CATGACTAAATTTGGCAGAAAGCATTAATTTATTTTGGAGACATTTTTCAGCAA	4864
DB	2774	CATGACTAAAGACAGAGACATTAATTTA--TTTGGAGACATTTTTCAGCTA	2825
RESULT 15			
XX	AA141577		
XX	AA141577	standard; CDNA; 3260 BP.	
XX	AA141577;		
XX	19-APR-2002	(first entry)	
XX	DE	Murine MEK1-1 coding sequence.	
XX	Mouse; MEK1; mitogen ERK kinase kinase; enzyme; cancer; neuroprotective;		
XX	autoimmune disease; signal transduction; allergy; inflammation;		
XX	neurological disorder; hormone-related disease; apoptosis; infection;		
XX	cytosolic; immunosuppressive; antiinflammatory; antiallergic; gene;		
XX	neotropic; antiparkinsonian; contraceptive; ss.		
XX	Mus musculus.		
XX	OS		
XX	Key	Location/Qualifiers	
XX	FT	486..2504	
XX	CDS	/*tag= a	
XX	FT	/product= "MEK1.1"	
XX	FT		
XX	PN	US633170-B1.	
XX	PD	25-DEC-2001.	
XX	PE	05-APR-1996; 96US-0628829.	
XX	PR	15-APR-1993; 93US-0049254.	
XX	PR	14-OCT-1994; 94US-0333460.	
XX	PR	12-MAY-1995; 95US-0440421.	
XX	PR	06-JUN-1995; 95US-0472934.	
XX	PA	(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.	
XX	PI	Johnson GL;	
XX	XX	WPI: 2002-163179/21.	
XX	DR	P-PSDB; AAM48934.	
XX	DR		
XX	PT	New isolated nucleic acid encoding mitogen extracellular	
XX	PT	signal-regulated kinase kinase, useful for gene therapy of e.g. cancer	
XX	PT	and for recombinant protein production	
XX	PS	Claim 1; Column 101-108; 125pp; English.	
XX	XX		
XX	CC	The present invention provides the protein and coding sequences of a	
XX	CC	number of murine mitogen extracellular signal-regulated kinase (ERK)	
XX	CC	kinase kinase (MEKK) enzymes. The sequences can be used to treat a wide	
XX	CC	range of diseases including cancer, autoimmune diseases, inflammation,	
XX	CC	allergies, degenerative neurological diseases and hormone-related	
XX	CC	diseases, and for inhibiting spermatogenesis or oocyte maturation for	
XX	CC	contraception. The present sequence is the murine MEKK1.1 coding	
XX	CC	sequence.	
XX	SO	Sequence 3260 BP; 869 A; 837 C; 793 G; 761 T; 0 other;	
QY	Query Match	37.3%; Score 1955.6; DB 24; Length 3260;	
QY	Best Local Similarity	82.7%; Pred. No. 0;	
QY	Matches 2376; Conservative	0; Mismatches 444; Indels 54; Gaps 10;	
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DB	1	TACATCTCTTTCGACAGTCTGGCAGAAAGATCAAACTTCAGAGACTTCCGGCCAGTT	60

[illegible]

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Db	1215	GATCTGGCACTGTCTCCAGGTGTGAGCAAGCTTTGGCGGGCGGCAACAGTGGCAAC	1274
QY	3316	GCTGTTATACCACTGACGAGACAGTGTCAACCCAGTAGAGGAGAAATAGCAGATTAGAT	3375
Db	1275	GCCGTCATACCCAGCAGAGAGAGAGTGTACGCCGGTGGAGGACAAAGTAGGATTAGAT	1334
QY	3376	GTCATTAACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAAAGCATCTATGCTTCAAGT	3435
Db	1335	GTGAACACCGAGCTCAACTCCAGATTCGAGACCTTCTTGAAAGCATCCATGCTTCAAGT	1394
QY	3436	GATTAACAAGTAACCTTTTAAGTAGAAGTGTGCTCTGCTCCCTGAAAAGGCTGAATAAT	3495
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Db	1515	GAAAGGAGGAGGCTTTTAGCATTCGCTCCATGGCATGTCAAGCGCTTCAGATATCCCTCCC	1574
QY	3616	ATAGTTCTCTCAGCTGCAGAGTGTGAATAATGAGAAGATATCATTTATTAACAGATACA	3675
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QY	3736	CTGAAAGGTCAAAGATAGGCTTTGGAGCATTTCTTCTGTTATACAGGCTCAAGATGTG	3795
Db	1695	CTGAAAGGCCAGAGATAGGCTTCGAGCATTTCTTCTGTTATACCAAGCACAGATATGTG	1754
QY	3796	GGAATGGAACTTATATGCTGTTAAACAGGTGACTTATGTAGAAACATCTTCTGAG	3855
Db	1755	GGGATGTGGAACTTATATGCGTGTGAAACAGGTGACGTAGTAAGAACATCTCTCCGAG	1814
QY	3856	CAAGAAGAAGTAGTAAGAAAGCACTAAGAAGAAATAGAAATGATGACCATCTGAAATCAT	3915
Db	1815	CAGAGAGAGGTGGTGGAAAGCTTGAAGGAAGAAATCCGATATATGGTATCCTCAACAT	1874
QY	3916	CCAAACATCATTTAGCATGTTGGGAGCCAGCTGTGAAAGAAAGCAATTAACATCTCTTCATT	3975
Db	1875	CCAAACATCATTCGAGTGTGGGGGCCAGCTGGGAGAAGCACTACAACTCTTCATT	1934
QY	3976	GAAATGATGGCAGGGGGAATGGGTGCTCATTTTCTAGTAATAATAGGACCTTCAAGAA	4035
Db	1935	GAGTGGATGGGGGAGGATGTGTGCTCATCTTTAGTAATAAGGACCTTCAAGGAG	1994
QY	4036	TCAGTAGTTATTAACTCACTGAAACAGTTACTCCGGGCGCTTCCGATCTCCATCCATAAAC	4095
Db	1995	TCATCTGCTCAATTAACTCACTGAGCAAGTTATCTGGCGCTTCTCTATCTCCAGAGAAAC	2054
QY	4096	CAAAATCTCAAGAGATGTCAAAAGGTGCCAATTGTCTAATTAGACAGCACTGGTCAAGAA	4155
Db	2055	CAGATCAATTCACAGAGACGTCAAAAGGTGCCAACCTCTATTGACAGCACCGGTACAGG	2114
QY	4156	CTAAGATTTGCAATTTTGGAGCTGCAGCAGAGTTGGGATCTCAAAAGAACTGTGTGACAGA	4215
Db	2115	CTGGAATTTGACCTTTTGGAGCTGTGCGAGGTGTGGCATCAAAAGAAACGGTGTGACAGA	2174
QY	4216	GAGTTTACAGGACAAATTAAGTGGGAGCAATTTGCAATTTATGGCACTGAGATCTAAAGAGT	4275

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Db 2175 GAATTCAGGGAGACGTTACTGGGGACAAATTCATTCATGCGCGCTGAGGTCCTAAGAGCT 2234
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Db 2235 CACGACTATGTGTAGAGCTGTGATGTATGGAGTGTGGCTGTGCGCATTTATAGAAATGCT 2294
OY 4336 TGTGCAAAACCAACCATGTGAATGCAAAAAACACTCCCAATCATCTGCTTGATTTAAG 4395
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OY 4396 ATTGCTAGTCACTACTGCTCCATGATGCTCCCTTACATTTGTCCTGGTTTACGAGAT 4455
Db 2355 ATTGCTAGGCAACTACTGCACTGCACTCCCTGCTCACACCTGTCCCGGCTGTGCGGAC 2414
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Db 2415 GTGGCGGTGGCTGTGTAGAACTTCAAGCTCAGAGCGGCTCGCTCCAGAGAGACTGCTG 2474
OY 4516 AAGCATCCACTCTTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4575
Db 2475 AAGCATCCCGGTCTTCCGTACAGCTGTGATGATGATGATGATGATGATGATGATGATG 2534
OY 4576 AGGATGCTCAACAAGAAAAAACTTG---TGGGGAACCAATGATATTCTACTG 4631
Db 2535 AGGATATCGAAGCGGAGAGAGAAAGAACTTGTGGCGACCATGCGCTAACCAG 2594
OY 4632 CCATGATGCCACTGAACTGATGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 4691
Db 2595 CCTCAAGCCACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 2653
OY 4692 ATTGACAAATCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 4750
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OY 4751 ACTGTAACCTGTGCTTCAAAAGAACTGGCCCTAGTGAACAGAAAAAATGAAGTTG 4810
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OY 4811 CATGACTAAATTCAGAGCATTAATTTATTTTGTGAGCAGCTTTTTCAGCAA 4864
Db 2774 CATGACTAAAGAACAGAGCATTAATTTA--TTTTGAGCAGCTTTTTCAGCTA 2825

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Search completed: December 27, 2002, 16:58:43
 Job time : 1028 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:44 ; Search time 32 Seconds

(without alignments)
4542.351 Million cell updates/sec

Title: US-09-697-898-2

Perfect score: 7825

Sequence: 1 MAAAGNRRSSSGFPGARAT.....PDRPPSRRLKHPVRRITW 1512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6892.5	88.1	1493	2 T10757	MAP kinase kinase
2	3172.5	40.5	687	2 A46212	MEK kinase - mouse
3	619	7.9	1478	2 S20117	protein kinase BCK
4	595.5	7.6	706	2 A48084	STREII protein kina
5	591.5	7.6	651	2 A96591	NPK1-related prote
6	552.5	7.1	1338	2 T30565	MAP kinase kinase
7	543.5	6.9	659	1 A39723	protein kinase byr
8	538.5	6.9	883	2 A96662	hypothetical prote
9	535	6.8	738	1 A51380	protein kinase STE
10	531.5	6.8	608	2 G96575	probable MEK kinas
11	517.5	6.6	1116	2 T38073	serine/threonine-p
12	502.5	6.4	1607	2 T03022	MAP kinase kinase
13	484	6.2	652	2 H86221	hypothetical prote
14	483	6.2	582	2 T51625	MAP3k alpha protei
15	461.5	5.9	608	2 T01833	serine/threonine-s
16	455.5	5.8	650	2 J04673	protein kinase (EC
17	449.5	5.7	535	2 T51736	mitogen-activated
18	447	5.7	773	2 T01835	serine/threonine-s
19	446	5.7	372	2 T52621	mitogen-activated
20	445.5	5.7	560	2 D85084	probable mitogen-a
21	436.5	5.6	572	2 T01836	serine/threonine-s
22	433.5	5.5	1401	2 T39225	MAP kinase kinase
23	429.5	5.5	1379	2 J05778	apoptosis signal-r
24	426	5.4	560	2 T14616	hypothetical prote
25	423	5.4	372	2 T02550	NPK1-related prote
26	423	5.4	1579	2 S59801	protein kinase SSK
27	415	5.3	1387	2 T16511	hypothetical prote
28	413.5	5.3	1288	2 J00363	mitogen-activated
29	410	5.2	836	2 B96716	probable serine/th

30	409.5	5.2	1895	2 T06609	disease resistance
31	399	5.1	471	2 T39232	probable serine th
32	398.5	5.1	658	2 T39500	serine/threonine-s
33	392	5.0	756	2 T50298	MAP kinase kinase
34	389.5	5.0	403	2 J05974	autora-related kin
35	388.5	5.0	939	2 S28394	probable serine/th
36	385	4.9	525	2 S58682	protein kinase, p2
37	380.5	4.9	339	2 C86185	hypothetical kinase
38	380.5	4.9	658	2 S60170	hypothetical prote
39	377.5	4.8	544	2 A57597	protein kinase Pak
40	377.5	4.8	544	2 S40482	beta-p21-activated
41	377.5	4.8	545	2 G01773	serine/threonine-s
42	377.5	4.8	1418	2 T15232	p21-activated prot
43	373.5	4.8	1062	2 S46367	hypothetical prote
44	373.5	4.8	1230	2 T18259	protein kinase CDC
45	373	4.8	1230	2 T18256	serine/threonine p
					probable serine/th

ALIGNMENTS

RESULT 1

T10757
MAP kinase kinase (EC 2.7.1.-) 1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence #revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10757

R:Xu, S.; Robbins, D.J.; Christerson, L.B.; English, J.M.; Vanderbilt, C.A.; Cobb, M.
Proc. Natl. Acad. Sci. U.S.A. 93, 5291-5295, 1996

A:Title: Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-associated 1

A:Reference number: Z17123; MUID:96224276; PMID:8643568

A:Accession: T10757

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1493 <XUS>

A:Cross-references: EMBL:U48596; NID:91354136; PID:NAC52596.1; PID:g1354137

C:Genetics:

A:Gene: MEK1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP; phosphotransferase; protein kinase

Query Match	88.1%	Score 6892.5	DB 2	Length 1493
Best local similarity	89.2%	Pred. No. 7e-232		
Matches 1350; Conservative 45; Mismatches 96; Indels 23; Gaps 8;				
Qy	1	MAAAGNRRSSSGFPGARATSPDAGGCGALAKASSAPAAAGLIREAGSGGERADWRR	60	
Db	1	MAAAGDRASSSGFPGAAASPEAGGCGALQSGAPAAAGLIRETSAGERRADWRRQ	60	
Qy	61	QLRKRVSELDQLEPQPLFLAASPASTSPSPADAAAGSGTGFPYAVPPHGAASRG	120	
Db	61	QLRKRVSELDQLEPQPLFLAASPASTSPSPADAAAGSGTGFPYAVPPHGAASRG	120	
Qy	121	GAHLTESVAAPDSGASPPAAAPGKRAAPAPGEMENKKTGLHMDRPP	180	
Db	121	GSASLELAARSGASPPGAP-----PS-AAAPSGEMENKKTGLHMDRPP	170	
Qy	181	EERMIREKLAKTQMPAMKHEWLERRRNRGPVYKPIPAKGDSENNHLLAESPEGEVQASA	240	
Db	171	EERMIREKLAKTQMPAMKHEWLERRRNRGPVYKPIPAKGDSENNHLLAESPEGEVQASA	230	
Qy	241	ASPASKGRSPSPGSGRTVKSSEPGVRRKRVSPVPOSGRIIPPRADSPDGFSPYS	300	
Db	231	AAAPAKGRSPSPGSGRTVKSSEPGVRRKRVSPVPOSGRIIPPRADSPDGFSPYS	290	
Qy	301	PEETRRVNVKWARLYLLOQIGPNSFLIGGSPGNKRVFIPGPNCGSCARFCIHLF	360	
Db	291	PEETSRVNVKWARLYLLOQIGPNSFLIGGSPGNKRVFIPGPNCGSCARFCIHLF	350	
Qy	361	VMLRVFOLESPDMLRRTLKNEVESLFQKYHSRRSSRIKAPSNTIOTKFSRMSNHT	420	
Db	351	VMLRVFOLESPDMLRRTLKNEVESLFQKYHSRRSSRIKAPSNTIOTKFSRMSNHT	410	

OY	421	LSSTSTSSSENIRKDEEOMCPICLGLMLDEESTLVEEDGRNKLHHHCHSINAEBR	480
Db	411	LSSTSTSSSENIRKDEEOMCPICLGLMLDEESTLVEEDGRNKLHHHCHSINAEBR	470
OY	481	RNRREPLICPLCRSKWRSHDFYSHELSLSPVSPSSLAAOQVVOOPPLGGS--RRNDESNF	539
Db	471	RNRREPLICPLCRSKWRSHDPTSHELSLSPVSPSSLAAOQVVOOPPLGGS--RRNDESNF	530
OY	540	NLTHYGTQOJDIPAYKDLAEPMIOVFGMELVGLCFSRNMVNRREMLRRLSHDVSAGALLAN	599
Db	531	NLTHYGTQOJDIPAYKDLAEPMIOVFGMELVGLCFSRNMVNRREMLRRLSHDVSAGALLAN	590
OY	600	GESTGNSSGSSGSSPSCGAITSSSQTSISGDVYEAACCSYLSMYCADPYKYVYALKTR	659
Db	591	GESTGTSGSGSGGSLISAGAASSGSSPSISGDVYEAFCYSYIYICADPYKYVYALKTR	650
OY	660	AMLYVTPCHSLAEIKIOLRLLDPVDTILYKCADANSRTSOLISITLLELGGAGELAV	719
Db	651	AMLYVTPCHSLAEIKIOLRLLRPVDTILYKCADANSRTSOLISITLLELGGAGELAV	710
OY	720	GREILKAGSITIGGVADVIVLNCILNQTESNNMOELLGRICLIDLRLLEPAEFYPIYST	779
Db	711	GREILKAGSIGGVADVIVLSCILNQAESNNMOELLGRICLIDLRLLEISAEPYPIYST	770
OY	780	DVSOAPEPEIYKKLLSLFLPALDSIDNSIMYKGLSRIRYIYSSAMVTPVHYFSKLE	839
Db	771	DVSOAPEPEIYKKLLSLFLFALDSIDNSIMYKGLSRIRYIYSSAMVTPVPLESKLT	830
OY	840	MLSYSSHTFPMRRMRMLAIADEVEITAEALIQLEVEPTLGGQOOSFLOASVPMNYLETETN	899
Db	831	MLSYSSGSHFPMRRMRMLAIADEVEITAEALIQLESEDTLGGQOOS--SQALAPPY--PES	886
OY	900	SSPECTVHLEKTKGKGLCATKILSASSEDISERLASISVG--PSSSTTTTTTTTTPOKPMOYT	958
Db	887	SSLEHTAVERTKGLCATATRLSASSEDIDRLAGVSGULPSSA-----TTQOKPMOYT	940
OY	959	KGRPHSQCINSSPLSHHSQMLPALSTPSSSTPSVPAQNTIDVSKIRLOGITPCRIPSAS	1016
Db	941	KGRPHSOCINSSPLS--PQMLFPAISAPCSSASVAGSVTADSKRPHAPFAPCKIPISAS	999
OY	1019	POTORKFSLQHRMCRPNKMDKLSPVFNQSRPLPSNNIHRPKRSPRGTNNSKOGDPBK	1078
Db	1000	POTORKFSLQHRMCRPNKMDKLSPVFNQSRPLPSNNIHRPKRSPRGTNNSKOGDASK	1055
OY	1079	NSMTLDLNNSSKCDSDSGCSSNSSNAVIPDEVEFTPVBEKCRILDVNTLANSIEDLEA	1136
Db	1060	NSMTLDLNNASQCDSDSGCSSNSSNAVIPBEETAFPAEDKCKLDVNPENLSIEDLEA	1111
OY	1139	SMPSDDTVYTFKSEVAVLSPEKAEENDTYADVDYNNHOKCKEKEAEEBEALAIAMASMS	1196
Db	1120	SMPSDDTVYTFKSEVAVLSPEKAEESDPTYKDVDYNNHOKCKEKEAEEBEALAIAMASMS	1179
OY	1199	QDALPIYPOLOVENGEIDITIIIOOTPTLGHKAKOYREDEEMWIKGOOIGIGAFSSCY	1255
Db	1180	QDALPIYPOLOVENGEIDITIIIOOTPTLGHKAKAEYREDEEMWIKGOOIGIGAFSSCY	1233
OY	1259	QAOBDVGTCLAAVQVYVYNTSSEGEBEVEALREELRMMSHLNHNPIIRMLGATCEKSN	1318
Db	1240	QAOBDVGTCLAAVQVYVYNTSSEGEBEVEALREELRMMSHLNHNPIIRMLGATCEKSN	1299
OY	1319	YNLFLEWAGGSVAHLLSKGAERESVYINYTEOLLRGLSYIHNENIHRDYKGANLLID	1376
Db	1300	YNLFLEWAGGSVAHLLSKGAERESVYINYTEOLLRGLSYIHNENIHRDYKGANLLID	1359
OY	1379	STGQRLRIADIGAARARLASKGTGAGEGQGLGTIAFMAPEVYLRGOYGRSCDWSYGCA	1433
Db	1360	STGQRLRIADIGAARARLASKGTGAGEGQGLGTIAFMAPEVYLRGOYGRSCDWSYGCA	1411
OY	1439	IIEMACAPPPNNAKHSNHLALFKIASATTAJSTPSHLSPLGRDVALCLLELODDRPP	1496
Db	1420	IIEMACAPPPNNAKHSNHLALFKIASATTAJSTPSHLSPLGRDVALCLLELODDRPP	1477
OY	1499	SRELLKHPVFTTW 1512	

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DB      1480  SRELLKHEVFRTTW 1493
|||||
RESULT 2
A46212
MEK kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-May-1999
C:Accession: A46212
R:Langre-Carter, C.A.; Pleiman, C.M.; Gardner, A.M.; Blumer, K.J.; Johnson, G.L.
Science 260, 315-319, 1993
A:Title: A divergence in the MAP kinase regulatory network defined by MEK kinase and
A:Reference number: A46212; MUID:93227040; PMID:8355802
A:Accession: A46212
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-687 <LAN>
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBI:P:129292)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP
F:416-683/Domain: protein kinase ATP-binding motif
F:424-432/Region: protein kinase ATP-binding motif

Query Match          40.5%; Score 3172.5; DB 2: Length 687;
Best Local Similarity 89.5%; Pred. No. 2.4e-103;
Matches 628; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY      811  MWGKLRRRIYLSARNAVTVPHVFSKLEMLSVSSSTHFTMRRLMAIADEVEIAEAIQ 870
DB      1  MWGKLRRRIYLSARNAVTVPAVAFSKLVTLMLASGSTHFTMRRLMAIADEVEIAEYIQ 60

QY      871  LGVEPTLDGQDSFIQASVPNNYLETENSSPECTVHLEKGGKGLCATKSLASSSEDISER 930
DB      61  LGVEPTVGHGDDS--LQAAVAPTSCL---ENSSLEHTVHREKKGKGLSATRLSASSEDISDR 116

QY      931  IASISVGSSSTTTTTHTEBPKPMVOTKGRPHSCNLSPLSHSLOMFALTPSSST 990
DB      117  LAGVSVGLPSS-----TTBQPKPAVOTKGRPHSCNLSPLS--HAQMFAPSPAPSSA 170

QY      991  PSVPAGTATDVSKHRLQGFICRIRPSASPOQRKFSLOFHNRCENKDKSLSEVFTQSR 1050
DB      171  PSVP-----DISKHRLQAFVFCRKIPASPOQRKFSLOFQNCSEHRSRDSLSVFTQSR 225

QY      1051  PLPSSNIRPKPRSRPTPENTSKOGDPKNSMTLDLNSSSCKDDSGCCSSNSNAVIDSDE 1110
DB      226  PPPSSNIRPKPRSRVPSTSKLGATKSSMTLDLGSASRCDSDSGGCGGAGNAVIDSDE 285

QY      1111  TYFTVEEKKCRADVTEELNSSIEDLEASMPSSDPTVYFKSEVAVLSPEKENDDTYKDD 1170
DB      286  TYFTVEEKKCRADVTEELNSSIEDLEASMPSSDPTVYFKSEVAVLSPEKENDDTYKDD 345

QY      1171  VNHQCKEKEKAEDEEALAIAMAMASASQDLPIYPOQLVNGEDIILIQDTEPTLPGH 1230
DB      346  VNHQCKEKEKAEDEEALAIAMAMASASQDLPIYPOQLVNGEDIILIQDTEPTLPGH 405

QY      1231  TKAKPRPYEDTBWMLKGQOIGIGASSCTQADQVGTGLTMAVKQTYVANTSSDEEVEYEA 1290
DB      406  TKAKPRPYEDTBWMLKGQOIGIGASSCTQADQVGTGLTMAVKQTYVANTSSDEEVEYEA 465

QY      1291  LREELRMKSHLNHPRIITMLGATCEKSNYNLTIEEMAGSVAHLISKYGAKESVINYT 1350
DB      466  LREELRMKSHLNHPRIITMLGATCEKSNYNLTIEEMAGSVAHLISKYGAKESVINYT 525

QY      1351  EQLLGLSLYLEHNOYIIRHDVGKANLLIDSTQRLTIADFGAAARLASKGTAGCFQGLL 1410
DB      526  EQLLGLSLYLEHNOYIIRHDVGKANLLIDSTQRLTIADFGAAARLASKGTAGCFQGLL 585

QY      1411  GTIAFMADBEVLRGQOYGRSCDVWSYGCAITEMACAKPPWNAEKSHNLALFKTASATTA 1470
DB      586  GTIAFMADBEVLRGQOYGRSCDVWSYGCAITEMACAKPPWNAEKSHNLALFKTASATTA 645

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0Y 1471 PSTPSHSLPGLRDVALRCLELQPDQRRPSSRELLKHPVRRFTW 1512
 Db 646 PSTPSHSLPGLRDVALRCLELQPDQRRPSSRELLKHPVRRFTW 687
 RESULT 3
 S20117
 protein kinase BCK1 (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein J0906; protein kinase SUK1; protein kinase SSP31; protein YJL099
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 23-Apr-1993 #sequence.revision 23-Apr-1993 #text.change 24-Sep-1999
 C:Accession: S201117; S50298; S22285; S19061; JQ1432; S56872; S30794; JQ1118
 R:Crossligan, C.; Gehring, S.; Snyder, M.
 M: Cell. Biol. 12, 1162-1178, 1992
 A:Title: A synthetic lethal screen identifies SUK1, a novel protein kinase homolog implicated in the regulation of cell growth
 A:Reference number: S20117; MUID:92186847; PMID:1545797
 A:Accession: S20117
 A:Molecule type: DNA
 A:Residues: 1-1478 <COS>
 A:Cross-references: EMBL:M84389
 A:Experimental source: strain S288C
 R:Moisga, T.; Boles, E.; Schaaff-Gerstenschlaeger, I.; Schmitt, S.; Zimmermann, F.K.
 Yeast 10, 1481-1488, 1994
 A:Title: Sequence and function analysis of a 9.74 kb fragment of *Saccharomyces cerevisiae* chromosome V
 A:Reference number: S50295; MUID:93176706; PMID:7871887
 A:Accession: S50298
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-1478 <MIO>
 A:Cross-references: EMBL:X77923; NID:9640004; PIDN:CAA54896.1; PID:9640009
 R:Lee, K.S.; Levin, D.E.
 M: Cell. Biol. 12, 172-182, 1992
 A:Title: Dominant mutations in a gene encoding a putative protein kinase (BCK1) bypass the requirement for a second mutation in the 5' region of the gene
 A:Reference number: S22285; MUID:92107166; PMID:1729597
 A:Accession: S22285
 A:Molecule type: DNA
 A:Residues: 1-56, 'Y', 60-1478 <LEE>
 A:Cross-references: EMBL:X60227
 A:Experimental source: strain EG123
 R:Lee, K.S.; Levin, D.E.
 submitted to the EMBL Data Library, June 1991
 A:Description: An extragenic suppressor of mutations in the *S. cerevisiae* protein kinase BCK1
 A:Reference number: S19061
 A:Accession: S19061
 A:Molecule type: DNA
 A:Residues: 1-58, 'I', 60-263, 'P', 265-278, 'I', 280-702, 'S', 707-708, 'KP', 714, 'VITME', 715-79
 A:Cross-references: EMBL:X60227; NID:93414; PIDN:CAA42788.1; PID:93415
 A:Experimental source: strain EG123
 R:Rifke, K.; Araki, H.; Oshima, Y.
 Gene 108, 139-144, 1991
 A:Title: A new protein kinase, SSP31, modulating the SMP3 gene-product involved in plasma membrane function
 A:Reference number: JQ1432; MUID:92104496; PMID:1840547
 A:Accession: JQ1432
 A:Molecule type: DNA
 A:Residues: 149-1478 <IRI>
 A:Cross-references: EMBL:D10389; DDBJ:D90446
 R:Moisga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chaltatzis, N.; Fournier, R.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56855
 A:Accession: S56872
 A:Molecule type: DNA
 A:Residues: 1-1478 <MIV>
 A:Cross-references: EMBL:Z49370; NID:91008269; PIDN:CAA89389.1; PID:91008270; MIPS:YJL099
 R:Cusick, M.E.
 submitted to the EMBL Data Library, March 1992
 A:Reference number: S27437
 A:Accession: S30794
 A:Molecule type: DNA
 A:Residues: 602-959, 'R', 961, 'R', 963-1085, 'V', 1087, 'SLTIAHT', 1092-1094, 'RMD', 1101, 'TV', 1102-1103, 'V', 1104-1105, 'V', 1106-1107, 'V', 1108-1109, 'V', 1110-1111, 'V', 1112-1113, 'V', 1114-1115, 'V', 1116-1117, 'V', 1118-1119, 'V', 1120-1121, 'V', 1122-1123, 'V', 1124-1125, 'V', 1126-1127, 'V', 1128-1129, 'V', 1130-1131, 'V', 1132-1133, 'V', 1134-1135, 'V', 1136-1137, 'V', 1138-1139, 'V', 1140-1141, 'V', 1142-1143, 'V', 1144-1145, 'V', 1146-1147, 'V', 1148-1149, 'V', 1150-1151, 'V', 1152-1153, 'V', 1154-1155, 'V', 1156-1157, 'V', 1158-1159, 'V', 1160-1161, 'V', 1162-1163, 'V', 1164-1165, 'V', 1166-1167, 'V', 1168-1169, 'V', 1170-1171, 'V', 1172-1173, 'V', 1174-1175, 'V', 1176-1177, 'V', 1178-1179, 'V', 1180-1181, 'V', 1182-1183, 'V', 1184-1185, 'V', 1186-1187, 'V', 1188-1189, 'V', 1190-1191, 'V', 1192-1193, 'V', 1194-1195, 'V', 1196-1197, 'V', 1198-1199, 'V', 1200-1201, 'V', 1202-1203, 'V', 1204-1205, 'V', 1206-1207, 'V', 1208-1209, 'V', 1210-1211, 'V', 1212-1213, 'V', 1214-1215, 'V', 1216-1217, 'V', 1218-1219, 'V', 1220-1221, 'V', 1222-1223, 'V', 1224-1225, 'V', 1226-1227, 'V', 1228-1229, 'V', 1230-1231, 'V', 1232-1233, 'V', 1234-1235, 'V', 1236-1237, 'V', 1238-1239, 'V', 1240-1241, 'V', 1242-1243, 'V', 1244-1245, 'V', 1246-1247, 'V', 1248-1249, 'V', 1250-1251, 'V', 1252-1253, 'V', 1254-1255, 'V', 1256-1257, 'V', 1258-1259, 'V', 1260-1261, 'V', 1262-1263, 'V', 1264-1265, 'V', 1266-1267, 'V', 1268-1269, 'V', 1270-1271, 'V', 1272-1273, 'V', 1274-1275, 'V', 1276-1277, 'V', 1278-1279, 'V', 1280-1281, 'V', 1282-1283, 'V', 1284-1285, 'V', 1286-1287, 'V', 1288-1289, 'V', 1290-1291, 'V', 1292-1293, 'V', 1294-1295, 'V', 1296-1297, 'V', 1298-1299, 'V', 1300-1301, 'V', 1302-1303, 'V', 1304-1305, 'V', 1306-1307, 'V', 1308-1309, 'V', 1310-1311, 'V', 1312-1313, 'V', 1314-1315, 'V', 1316-1317, 'V', 1318-1319, 'V', 1320-1321, 'V', 1322-1323, 'V', 1324-1325, 'V', 1326-1327, 'V', 1328-1329, 'V', 1330-1331, 'V', 1332-1333, 'V', 1334-1335, 'V', 1336-1337, 'V', 1338-1339, 'V', 1340-1341, 'V', 1342-1343, 'V', 1344-1345, 'V', 1346-1347, 'V', 1348-1349, 'V', 1350-1351, 'V', 1352-1353, 'V', 1354-1355, 'V', 1356-1357, 'V', 1358-1359, 'V', 1360-1361, 'V', 1362-1363, 'V', 1364-1365, 'V', 1366-1367, 'V', 1368-1369, 'V', 1370-1371, 'V', 1372-1373, 'V', 1374-1375, 'V', 1376-1377, 'V', 1378-1379, 'V', 1380-1381, 'V', 1382-1383, 'V', 1384-1385, 'V', 1386-1387, 'V', 1388-1389, 'V', 1390-1391, 'V', 1392-1393, 'V', 1394-1395, 'V', 1396-1397, 'V', 1398-1399, 'V', 1400-1401, 'V', 1402-1403, 'V', 1404-1405, 'V', 1406-1407, 'V', 1408-1409, 'V', 1410-1411, 'V', 1412-1413, 'V', 1414-1415, 'V', 1416-1417, 'V', 1418-1419, 'V', 1420-1421, 'V', 1422-1423, 'V', 1424-1425, 'V', 1426-1427, 'V', 1428-1429, 'V', 1430-1431, 'V', 1432-1433, 'V', 1434-1435, 'V', 1436-1437, 'V

[illegible]


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Db 793 RESPTKPELA-PKRAPRANTSPORTLISTKONKPIRLVASTKITSN-----842
Qy 1034 PENKSDKLSPTVTOGRPLPSSNIHRP-KSRPTPGNTSKQDPSKNSMTL-----D 1084
Db 843 -----KRSKPLPQLSSPIEASSSPSDLSSTYTPASHVLIPQYKAND 889
Qy 1085 LNSSKCD-DSFCCSS-----NSSNAVPEDEIVF---TP-----VEEKRL 1122
Db 890 VMRLTDDSTSTSPSLKMKOKVNRNSNSTVSTNSIFSPSPDLKRGNSKRVVSTSA 949
Qy 1123 DVNTEINSSIEDLEASMP-----SSDTVPKSEVAV-----LSPEKEN 1163
Db 950 DIFEE-----NDITPADAPMPDSDSDSSSDIIMSKKKTAPETNNKMKDEKSDN 1004
Qy 1164 DDTYKDVNHNOKCKEKE-----AEEELALATAMASASODA 1201
Db 1005 SSTHSDIEFYDSQTDKMEKKMFRSPPEVYVGNLEKFPFRALMDKPIITGSIASPTSPKS 1064
Qy 1202 L-----PIVQLOVE-----NGEDITITIOQDP-----1224
Db 1065 LDSLSPKNVASSRTEPSTPSPVPPDSSEYETQDGLNGKNKPLNQAKTPKRTKRTITIA 1124
Qy 1225 -----ETLPGH-----TKAKQPYREDEE-WLKGOQIGIG 1252
Db 1125 HEASLARKNSVLIKRONTKMGTRMVEVTENHNVSTINKAKNSGGEYKKEPRAMKGMIGKG 1184
Qy 1253 AFSSCYQADVDGTGLMAVAKQVTVYNTSSEDEEV---VEALREIRMSHLNHPNITRM 1309
Db 1185 SGCAVYLCLNTVTGEMMAVAYQVE-VPKYSSQNSAIIISTVEALRSEVSTLKLIDLHNIYQY 1243
Qy 1310 LGATCKSNVNFIEEMAGSVANHLISKGAFESVYINTBELLGLSLHENOIIHRD 1369
Db 1244 LGEMNNNTYSLFELEVAGSGVSLRMGRFEPDEPKHILTYVGLGLALHSHKGLIHRD 1303
Qy 1370 VGANLILIDSTGQRILADIAGAARLASKGTGAGEFQGLGTIAFMAPEVLRCGOO-YGR 1428
Db 1304 MMADNLLDQDG-ICKISDFGISRK--SKDIYNS-DMMRGIVFPMAPMVPVTKQCYSA 1359
Qy 1429 SCQVMSVCAIIEMACAPRNAEKSNHLIAFKTASATTAPISPSHLSPLGRVALR- 1487
Db 1360 KVDIMWLGIVLEMFAGKRPWS---NLEVAAMFKIGKSKSAPPIEDTLISQIGRNF 1416
Qy 1488 ---CLELOPQDPRPSRELLKHP 1506
Db 1417 LDACEFINPEKRPANELLISHP 1438

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RESULT 4

```

A48084
SPELL protein kinase homolog NPRI - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 19-Dec-1997
C:Accession: A48084
R:Banno, H.; Hirano, K.; Nakamura, T.; Irie, K.; Nomoto, S.; Matsumoto, K.; Machida, Y.
Mol. Cell. Biol. 13, 4745-4752, 1993
A:Title: NPRI, a tobacco gene that encodes a protein with a domain homologous to yeast E
A:Reference number: A48084; MUID:93330268; PMID:8336712
A:Accession: A48084
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-706 <BAND>
A:Experimental source: BY-2 cells
A:Note: sequence extracted from NCBI backbone (NCBIN:135697, NCBI:135698)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP
F:94-358/Domain: protein kinase homology <KIN>
F:102-110/Region: protein kinase ATP-binding motif

```

```

Query Match 7.6%; Score 595.5; DB 2; Length 706;
Best Local Similarity 42.0%; Pred. No. 4,6e-14;
Matches 121; Conservative 60; Mismatches 94; Indels 13; Gaps 6;

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Qy 1227 LPHTRAKOP---YREDT---EMLKGOQIGLAFSSCYQADVGTGLMAVAKQVTVYRNT 1280
Db 74 LPSISKAELEPAKARKDPTPIRMRKGMICGAFGRVYMMAMNDSEGLAIKEYSIAMNG 133
Qy 1281 SSQD--EEVEALREIRMSHLNHPNITMLCATCKSNVNFIEEMAGSVANHLISKY 1338
Db 134 ASKRRQAHVRELEEEVNLKNSHPNIVYLTGARAGSLNITLFEVPGSSISLGLCKP 193
Qy 1339 GARFESVINYTEQLLGLSLYHENOIIHRDVGANLILIDSTGQRILADIAGAARLASK 1398
Db 194 GSFPESYIRMYTKQLLGLLEYLHKNGMHRDIGNANILVDNKG-CIKLADFGASKVVEL 252
Qy 1399 GTGAGFQGLQTLTIAFMAPEVLRGOQYGRSCVWSVCAIIEMACAPRNAEKSNHL 1458
Db 253 ATMTG--AKSMKGTPLYMAPEVILQTHSFSADISWVGCTIIEATGKPPWS--QOYQEV 308
Qy 1459 ALIFKIASATTAPISPSHLSPLGRVALRCLDLOPQDPRPSRELLKHP 1506
Db 309 ALFPHIGTYSHPPIRPHLSAESKDELLKCLQEPHLRHSASNLQHP 356

```

RESULT 5

```

A96591
NPRI-related protein kinase 2 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: A96591
R:Theologis, A.; Ecker, J.R.; Palm, C.T.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chen, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakao, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tello
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A96591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-651 <STO>
A:Cross-references: GB:A8005173; NID:g9857521; PIDN:AAG00876.1; GSPDB:GN00141
C:Genetics:
A:Gene: T24C10.7
A:Map position: 1
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

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Query Match 7.6%; Score 591.5; DB 2; Length 651;
Best Local Similarity 43.3%; Pred. No. 5,8e-14;
Matches 119; Conservative 55; Mismatches 90; Indels 11; Gaps 5;

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Qy 1234 KQPRDETEWLKQGLGAFSSCYQADVGTGLMAVAKQVTVYRNTSSQD--EEVEAL 1291
Db 63 KPIR-----WRKQOLIGRAGFGVYVGMNIDSEGLAVKOVLLTSCASKKQIAHIQEL 118
Qy 1292 REEIRMSHLNHPNITRMGATCEKSNVNFIEEMAGSVANHLISKYGFESVINYTE 1351
Db 119 EEEVKLLKNSHPNIVRYLGTAREDETLNLEFVPGSSISLLEKFAFPESVRYTYN 178
Qy 1352 QILRGSLYHENOIIHRDVGANLILIDSTGQRILADIFGAARLASKGTGAGFQGLG 1411
Db 179 QLLGLLEYLHNAIMHRDIGNANILVDNKG-CIKLADFGASKVAVLATISG--AKSMKG 235
Qy 1412 TIFMAPEVLRGOQYGRSCVWSVCAIIEMACAPRNAEKSNHLIAFKTASATTAP 1471
Db 236 TPTWMAPEVILQTHSFSADISWVGCTIIEATGKPPWS--QOYKELIAIFHIGTKSHP 293
Qy 1472 SIPSHLSPLGRVALRCLDLOPQDPRPSRELLKHP 1506
Db 294 PIPDNISNDANDELLKCLQEPHLRHSASNLQHP 328

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RESULT 6
 MAP kinase kinase kinase - yeast (Kluyveromyces marxianus var. lactis)
 C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T30565
 R:Jacob, J.D.; Kirchrath, L.; Gengenbacher, U.; Heinisch, J.J.
 J. Mol. Biol. 288, 337-352, 1999
 A:Title: Characterization of K1BK1, encoding a MAP kinase kinase of Kluyveromyces
 A:Reference number: 220862; MUID:99262846; PMID:10329146
 A:Accession: T30565
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1338 <JAC>
 A:Cross-references: EMBL:AA005079; NID:g3021328; PIDN:CAA06336.1; PID:g3021329
 C:Genetics:
 A:Note: BCK1
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 7.1%; Score 552.5; DB 2; Length 1338;
 Best Local Similarity 25.0%; Pred. No. 2.6e-12;
 Matches 211; Conservative 149; Mismatches 338; Indels 147; Gaps 32;

QY 741 ILGQTESNNMDELGLCLID-----RLLEFPAPFYHYSTDV-----SQAEPE 788
 DB 535 VKNASASNGEGSSDLTSDGSSHRRAVPQTPSHYDNTSAETDWSFKDSVPE 594
 QY 789 IRYKKLLSLTALQSDINSHMWKLSRRITLSSAMVTVVPHFSK-LLEMLSVSSST 847
 DB 595 IS-----DAHITLPKSRPRLKLNSSVLT--HASEKSTFRITRIOTSDT 636
 QY 848 HFTMRRLMALDEVEIAEAIQGVEDTLDGQDSFLQASVPNNYLETTENSPECTVH 907
 DB 637 DIDFNKRRESPPYVAELAK-RKAPKPVNG--NPVTSGLSPAAKNVSESLESPK 693
 QY 908 LEKTKGKL-----CATKLSA-----SSPDISELAIISVGPSSSTTTT 949
 DB 694 LDRNGKTIYKNNKPRPPPLTTERSSRRSVSSLSGQDINE--VKSPQVSFTPASTQV 749
 QY 950 EOPKP-----MVOTKGRPHSOCLNRP-----LSHSLMFPALSTP-----SSSTPS 992
 DB 750 MVRQPYGALETCLKPKSSADLSIRPRMSLRQFRRSSNSLNKRLKSLSTRQTLNTNSRPL 809
 QY 993 VPACTATDVSKHRLQGFIPCRIPSPQOTOKRFSLQFHRNCPENKDSKISP-----VFT 1047
 DB 810 VTSSTADIDENDISE-----ADAPELSDSDSYASASDEITWS 848
 QY 1048 QSRPLPSNTHRPKRPPTGNTSKQDPSKNSMTLDLNSSKCDSDFGSSNSN----- 1103
 DB 849 RDRKSISNDV--PEFSPTED-----TIDLVGDTTQVSVGATEGSDTPKRM 893
 QY 1104 AVIPSDVETTPVEKRCRLDVNTLANSIEDLEASMPSPDTVTYFKSEVAVLSPKAEK 1163
 DB 894 ALRSPVYVQNL-EKFPPLADLD-NPILGELTPPPSPNADSPSPRGPFKSLKTSEQ 951
 QY 1164 DDTYKDDVNNQK-----CKEKMEAEEDALAIAMASASQDALPIVQ-LQVEN-----GE 1214
 DB 952 QPAFLSSRGSSQFILTPEVKSILPKPKTKTKTRI-LAQEASERAKNEVSOQLORRKTMMGT 1010
 QY 1215 DIIIIQODTETPLPGHKAQPYREDTEMLKGOQIGLGAFFSCQAOQDVCGITLMAKQV 1274
 DB 1011 KVEITDKRTISLKNSSNRSKEYE-PAMIKGELITIGKSGFCAVVLALNVTTGEMLAYQV 1069
 QY 1275 TYVANTSEOE---EVEVALREETIRAMSHLNHPNIRMLGATCKESVNYLFIEMAGGSV 1331
 DB 1070 T-VPEFSQDESATSNWEALKSEVSTLKDLNHNVIQYLGEERKNNGIYSLPLEVYAGGSV 1128
 QY 1332 AHLISKAGRESVINYTEQLGLSYLHENOIIHNDVKANLLIDSTGRLRIADFGA 1391
 DB 1129 GSILRMAGRPDDOLIRHLTKQVLEGLAVIHSKGIHHRMCKADNLLDNDV-CRISDGI 1187
 QY 1392 AARLASGTAGGFGQGLGIAFMARVVL-RGOQYGRSCVMSVGCALIMACAPPMW 1450

DB 1188 SRKSNNTYSNS---DMTRGTVFMWAPMVDTPANGYSAKVDIWSLGCVLEMPAKRPWS 1244
 QY 1451 AEKSHNLALIFKIASATTPASIPSH---LSPGLRDVALRCLQDPDRPPRELKHP 1506
 DB 1245 ---NFEVVAANFQIGKSTAPIPDDTDFKDYLSPPAGQSLDQCFEIDPMRFTASIVGHP 1301
 QY 1507 VERTT 1511
 DB 1302 FCKTS 1306

RESULT 7
 A39723
 protein kinase byr2 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: protein kinase ste8
 C:Species: Schizosaccharomyces pombe
 C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 15-Sep-2000
 C:Accession: A39723; S30094; T39860; T40139
 R:Wang, Y.; Xu, H.P.; Riggs, M.; Rodgers, L.; Wigler, M.
 Mol. Cell. Biol. 11, 3554-3563, 1991
 A:Title: byr2, a Schizosaccharomyces pombe gene encoding a protein kinase capable of
 A:Reference number: A39723; MUID:51260705; PMID:2046669
 A:Accession: A39723

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-659 <MAN>
 A:Cross-references: GB:M74293; NID:g173352; PIDN:AAA35289.1; PID:g173353
 R:Styrkarsdottir, U.; Egel, R.; Nielsen, O.
 Mol. Gen. Genet. 235, 122-130, 1992
 A:Title: Functional conservation between Schizosaccharomyces pombe ste8 and Saccharom

A:Reference number: S30094; MUID:93062799; PMID:1435723
 A:Accession: S30094
 A:Molecule type: DNA
 A:Residues: 1-659 <STR>
 A:Cross-references: EMBL:X68851; NID:g5106; PIDN:CAA48731.1; PID:g5107
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21886

A:Accession: T39860
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-659 <MOO>
 A:Cross-references: EMBL:Z98270; PIDN:CAB10981.1; GSPDB:GN00067; SPDB:SPBC1D7.05C
 A:Experimental source: strain 972h; cosmid c1d7
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1997
 A:Reference number: Z21907

A:Accession: T40139
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 298-659 <MO2>
 A:Cross-references: EMBL:Z97211; PIDN:CAB10150.1; GSPDB:GN00067; SPDB:SPBC2F12.01
 A:Experimental source: strain 972h; cosmid c2F12
 C:Genetics:
 A:Gene: byr2; ste8
 A:Map position: 2

C:Superfamily: protein kinase byr2; protein kinase homology; SAM homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:1-66/Domain: SAM homology <SAM>
 F:392-658/Domain: protein kinase homology <KIN>
 F:400-408/Region: protein kinase ATP-binding motif

Query Match 6.9%; Score 543.5; DB 1; Length 659;
 Best Local Similarity 26.2%; Pred. No. 2.7e-13;
 Matches 181; Conservative 115; Mismatches 259; Indels 137; Gaps 27;

QY 871 LGVEDTLDGQDSFLQASVPNNYLETTENSPP-----EC---TVNLEKTKG---KGLCAT 918
 DB 46 LGINTATAGKQ--FLK---QRDYLR--EFPRLILRFATCNGQTRAVQSGRDYQKTLAIA 98
 QY 919 KLASSEDISERLASISVGPSSSTTTTTEQQRPMVOTGGRPHSOCLNPSLSHSQ 978
 DB 99 LKRFSLDASKFIVCV-----SSSRILKLTIEERKQI-----CFNSSSPERDLI 144

A:Cross-references: SGD:S0004354; MIPS:YLR362w
 A:Map position: 12R
 C:Superfamily: protein kinase byr2; protein kinase homology; SAM homology
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:38-104/Domain: SAM homology <SAM>
 F:434-733/Domain: protein kinase homology <KIN>
 F:442-450/Region: protein kinase ATP-binding motif

Query Match 6.8%; Score 535; DB 1; Length 738;
 Best Local Similarity 25.2%; Pred. No. 5.9e-12;
 Matches 205; Conservative 117; Mismatches 215; Indels 276; Gaps 35;

QY 781 VSOAPEVPEIRKRLSLTLFL-----QSINSHSNVGL-----SRRIYLSA----- 824
 DB 108 IEQVNRKKNLMKESVSLSTATLSNMSELIPKHCVIFILNDGSAKKVAVNCCFNADSIK 167
 QY 825 RMVTVPHVFESKLEMLSVSSSTHTFM-----RRRLMAIDVEVIAEALQGV 873
 DB 168 RLIRRLPH-----ELLATNSNGEYTKWVDYDFVLDYTKNVLHLTYDELVTICH--A 219
 QY 874 EDTLDGODSFLASVPPNNVLETTENSSPECTVHLEK--TGKICATKLSSASEDISER 930
 DB 220 NDRVE-----KNRLIFVSKDQTPS-----DKAISTSKLYLTLSALSG----- 258
 QY 931 LASISVGPSSSTTTTTTTEQPKPMVQTKGRPHS-----QCLNSSPLS 973
 DB 259 -----VPPSSSNL-----LAONKKGISHNNAEGKLIDNTEKDRIRQIFNQRP-- 300
 QY 974 HHSQMLPPLSTPSSSPVPAGTATDVKSKHRLGFTICRIRPSAPQQRKFSLOFHNC 1033
 DB 301 -----PSEFISTNLATGTFPHITDMKRLQ-----KWMRE----- 327
 QY 1034 PENKDSKLSFVQTQSRPL--PSSNIHRKPSRPTPGNTSKQGPSSKNSMTLDLSSSKC 1091
 DB 328 -SFRHSARLS--IAQRRLSAESNNI-----GD----- 352
 QY 1092 DDSGCSNNSNAVIPSDEYFTVEEKCRLDVTELNSSIEDLLEASMPSSDTTVFKS 1151
 DB 353 -----ILKHSNAV--DMALLOGIDQ-----TRLSKL-----DPT----- 381
 QY 1152 EVAVLSPEKKAANDPYKDDVHNOKCKEKEAEFEELALATAMASASODALPIYPOLOVE 1211
 DB 382 KIPPLAKRPPDNDALIS-----NOLELIVSEGE-----DHDF----- 417
 QY 1212 NGEDIILIIQODPTPELPGHTAKOPYREDTEMLKGOQIGLGFSSCYOADVGTGLMAV 1271
 DB 418 -GEISDLY-----SLP--TKIATP-----KWLKAGACIGSGSPGVYIGMAHNGELMAV 464
 QY 1272 KQTVTVRNT-----SSQOE-----VEALRE 1293
 DB 465 KOVEIKNNNIGVPTDNKQANSDENNEQEEQOEKIEDYGAVSHPTQNQNIHRKNVDALQH 524
 QY 1294 EIRMSHNLHPNIIIRMLGATCEKSNYNLFITEMAGGSVAHLISYGAKESEVINITYQOL 1353
 DB 525 EMLNLKEHLHEHNIVTYYGASQEGGNLTFLEYPGSVSSMLNNGPEESELITNFTQOI 584
 QY 1354 LRGLSYLHENQIIHRDVKAGMLIDSTGQRLIADFGAARLASKGTAGFEGOCILCTI 1413
 DB 585 LIGVAYLHKNNIHRDILKGANILIDING-CVKITDFGSKSLPLKNQNR--RASLOS 642
 QY 1414 AFMAPEVLRGQOYGRSCDVSVCALITEMACAKPPMAEKSHNLALIFKIASATPADSI 1473
 DB 643 FMSPEVAVKQATATKADIMSTCCVIVEMFGKHPE--PDFSQOALFKIGTNTT--PEI 698
 QY 1474 PSHLSPLGRDVALRCLQLQPODRPSPRELKHP 1506
 DB 699 PSMATSEGNFLKRAFELDIYRPSALELQHP 731

RESULT 10
 G96575
 Probable MEK kinase MAP3ka, 84794-81452 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 31-Mar-2001
 C:Accession: G96575
 R:Authors: A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alon
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G96575
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-608 <STO>
 A:Cross-references: GB:AE005173; MID:910645340; PIDN:AA621460.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F22G10.18
 A:Map position: 1

Query Match 6.8%; Score 531.5; DB 2; Length 608;
 Best Local Similarity 27.3%; Pred. No. 6.5e-12;
 Matches 145; Conservative 91; Mismatches 19; Indels 117; Gaps 17;

QY 1031 RNCPEKNDKLSPEVQTQSRPLPSSNIHRKPSRPTPGNTSKQGPSSKNSMTLDLSSSK 1090
 DB 8 KSC-KNKK-DNHRGILISTDRDKSSAVVDDPLTTRGCT-----PR 47
 QY 1091 CDDSEFGCSNNSNAVIPSDET-----VFPPV--EKCRLDVTELNSSIEDL--- 1135
 DB 48 CSREFAGASSAFSG-FDSDSTEKKCHPLRPLLSVSIHQDHVAGSGISVSASVSS 106
 QY 1136 -----LEASMPSSDTTVFKSVAVALSPEKKAANDPYKDDVHNOKCKEKEAEFE 1187
 DB 107 GSADDQSLVASRGRD--VKNVAAAPRSPERSV----- 139
 QY 1188 ALATIMASASODALPIYPOLOVENGEDIIITIOQT-----PETLPGH 1230
 DB 140 -----PRAATITTPPTPRHQRLSG--VSLSESTGNDRGSSSECHPLRPTPTS 191
 QY 1231 TKAKOPYRED-----TEWLKGOQIGLGFSSCYOADVGTGLMAVQTVTVRNT 1280
 DB 192 PSAYGSRIGGAYETSPSGFTWKKRFLGSETFGQVYLGFESEKGMKALKEVVISDD 251
 QY 1281 SSEOEVVEALREIRRMHSHLHPNIIIRMLGATCEKSNYNLFITEMAGGSVAHLISYGA 1340
 DB 252 QT-SKECLKOLNOEINLNOIOLCHPNIVGYGSELSSEETLSVLEYVSGSGSIHKLKLDYGS 310
 QY 1341 FKESVIVVYETDQLRLGLSYLHENQIIHRDVKGANLLIDSTGQRLIADFGAARLASG 1400
 DB 311 FTEPIQNTTQIOLGLAVLYHGRNTVHRDVKGANLLVDPNGE-IKLAFPGMAKHVTAYST 369
 QY 1401 GAGEFQGLLTIAFMAPEVLRGQO-YGRSCDVSVCALITEMACAKPPMAEKSHNLHA 1459
 DB 370 -----MLSEKSPYMAPEVAVMSQNGYHADVINSIGCTILEMATSKRPMW--QFE 421
 QY 1460 LIFKIASATPADSIPIPSHLSPLGRDVALRCLQLQPODRPSPRELKHPVFRRT 1511
 DB 422 AIFKIGNSKDPPEIPDHLSNDAKNFIRCLQRPNPTVPRPTASOLLEHPLRLNT 473

RESULT 11
 T38073
 serine/threonine-protein kinase mkl1 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 03-Dec-1999
 C:Accession: T38073
 R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL data library, April 1996
 A:Reference number: Z21767
 A:Accession: T38073

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1116 <CON>
 A:Cross-References: EMBL:270690; PIDN:CAA94620.1; GSPDB:GN00066; SPDB:SPAC1F3.02C
 A:Experimental source: strain 972h; cosmid c1f3
 C:Genetics:
 A:Gene: pmk1; SPDB:SPAC1F3.02C
 A:Map position: 1

Query Match 6.6%; Score 517.5; DB 2; Length 1116;
 Best Local Similarity 25.1%; Pred. No. 3.5e-11;
 Matches 185; Conservative 113; Mismatches 287; Indels 153; Gaps 25;

QY 859 INDEVEIAEIQGVEDTLDGQDSFLQASVPNNYLETENSPECTVHLE----- 909
 DB 424 LNSDFEITTA--GPNLSLSGHQ-----PDNKYYKGFSSAPNLAVELPSRRRGF 472
 QY 910 ---KTGKGLCATKLSASSEISERL-----ASISVSPSSSTTTT 946
 DB 473 EKRGAKEGEMATKILDATEQSEKKNFTYCRPHKVTLMKPLNLSGSSAPSPSSNTASV 532
 QY 947 TT-----TEQPKPVQTKGRPHSQCINSSPLSHNSQLMFPALSTPSSSTPVPAGTATD 1000
 DB 533 LTRNFVAHNDPPRPPTETSSLRKNTLTRRPSIRHAR-----SSPIYDTG-HNE 580
 QY 1001 VSKHRLQGITPCRIIPASQTKKESLQF-----HKNCEPNKSDKLSPVFTQSRP---- 1051
 DB 581 ASKFSHTSFDP--KASSKSSNSLKESEVALSELPEDAPALDESLSGDPFMAIQPKOSS 638
 QY 1052 --LPSSNIRHPKSRPTPGNTSKQDPSKNSMTLDNLSK-----C--DDSFCCSSNSN 1103
 DB 639 SQVPRKNHNIQSKLSI--NTEAATDLKANEL-----SSKPTREYGRGDRSISLPLST 651
 QY 1104 AVIPDETVFTVEEKCRLDVNTELNSSIEDLE-----ASMPSSD 1144
 DB 692 RLKSKHIRESPSSKVINSGNMEVRPSADLDYEDREFPRYDLDKVLVVDQSRMVSF 751
 QY 1145 TTYTTER---SEVAVLSPEKAENDTYKKDOYNNHQCKEKEAEERALAIAMMASQDA 1201
 DB 752 SKVSTPRKKSVALAREASE---ARKELRHNAKNNKSGNLRSSSTKLM----- 798
 QY 1202 LPTVLOQVENGEDI11IIOODTPETLPKHTKAKOPYREDETMKGOQIGLAESGQAO 1261
 DB 799 -----GSRIVELKPDITITSGSVSQNATFK---WAKGELIGNGTIGKPYFLAM 843
 QY 1262 DVGCTGLAAVKOYTVYRNTSS---OEVEVALREERIMSHLNHPNITRMGATCEKS 1317
 DB 844 NNTGELLAVKQVEIPQTINGRHQDLKDIVDSINAEISMIADLDLNTIVQYIGFEKTER 903
 QY 1318 NYNLFEEMAGGSVAHLLSKYGAFKESVYINTEOLLRGLSYLHENQIIRDOVKANLLI 1377
 DB 904 DISIFLEYSGSISGICLNNGCFEQLVRFVSKOVLAYGLSYLHSGIILHRDKADNLLI 963
 QY 1378 DSTGQRLRIADGAAARLASKGTAGEFOGOLGITYAFMAPEVLRL--OQYGRSCDVMVY 1435
 DB 964 DEDGV--CKISDGISKH--SDNYNDANDANLSMGSIFFWAPRYIHHDHQISAKYVWMSL 1020
 QY 1436 GCATITMACAKPPMAEKSNHLALIFKTASATTAPISPSHL---SPGLRDVALRCLEL 1491
 DB 1021 GCVVLEMLAGRRPWSYDE--AIQAMFKLGTEKKAPRIPSELVYSQSPKAIQFLNACFTV 1077
 QY 1492 OPDDRPSRELLKHPYFR 1509
 DB 1078 NADVRPTAEELLNHPMK 1095

RESULT 12
 T03022
 MAP kinase kinase - human
 C:Species: Homo sapiens (man)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Nov-1999
 C:Accession: T03022
 R:Takekawa, M.; Posas, F.; Salto, H.

submitted to the EMBL Data Library, May 1997
 A:Description: A human homolog of the yeast Sak2/Sak22 MAP kinase kinase kinase, MTK1
 A:Reference number: Z14824
 A:Accession: T03022
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1607 <TA>
 A:Cross-References: EMBL:AF002715; NID:92352276; PIDN:AAB68804.1; PID:92352277
 C:Genetics:
 A:Note: MTK1

Query Match 6.4%; Score 502.5; DB 2; Length 1607;
 Best Local Similarity 19.7%; Pred. No. 1.7e-10;
 Matches 288; Conservative 239; Mismatches 574; Indels 363; Gaps 59;

QY 169 TLKGLHMDRPREEMIREKIKATCPAMKHEML---ERRNRR----- 208
 DB 370 SLQALQKDYKRYAKAOFQDVAQLCL-----MLNTTKDLNQRLRMGYLGIKNLSDIG 423
 QY 209 GPVYVAPRIPYKGDSEMNHLAESPPEVOASAPASKGRSPSPGNSPGRTVKSESPG 268
 DB 424 WPFELIPSPSPSGNBEYEGDDTEGLKELSS-----TDESEBEQ 465
 QY 269 VRKRYSPVPEFGRTTPRRASPDPGFSPYSPETNRNRYKWRARLYLLOQIGRNSFL 328
 DB 466 ISDPVY-----PETROPDINSFDIQSRDCISK-----LERLESEDS 503
 QY 329 IGDSPDNKYRVFIPGONSCARGTFCIHLFVLMVLFQLEPDPMLVRKTLKNFVESL 388
 DB 504 LGMGARD-----WTEAG-FSRKCLTITYPFV-----DKALKQMKRL 542
 QY 389 FQKYHS-----RSSRIKAPSRNTIQFVRSMSNSHTLSSSTSTSSSE--NSIKDE 438
 DB 543 ILRLKLMDSIORARIALYKNDRPFESEFPDPMGSDVQLSRIPPSSEKCSAVSE 602
 QY 439 EEQMCIILLGMD---EESLVCEGDCGNKTH--HHCSTIAEECRNRREPLICPL-- 490
 DB 603 E-----LKAMDLPSEFPAFLV--CVLLNVJHECLKLEO--RPAGEPSLSTIQ 650
 QY 491 ---CRSKWRS-----HDFYSHELSPVDSPLSRAAOQTVQOOLPAGSRNOESNF 539
 DB 651 LVRECKEVLKGLMKQYQFMQLQVLEDEK-----DCNI 667
 QY 540 NLTHYGTQIPPAKYDLAEWIOV---GMLVCLFSRKN-----VR--EMAL 564
 DB 688 DAFEDLHKMLMYFPDMSWIOMLQOLPQASHLSKLNLEEMENFTKEITHYIRGSEAO 747
 QY 585 RRLSHVSGALLANGESTGNSGSSGSPSGATSGSSOTSTSGRVENCCLVSMYCA 644
 DB 748 GKLFCDIAGMLKSTGFLFEGIQESCAEFWTSADSSASDEITRSVIE-----ISRLAK 802
 QY 645 DPVYKVVVAALKTLRAMLVYTPCHSLAERIKILORLQPVVDI---LVKCADANSRTSQ 700
 DB 803 ELFEHRENRASKMLGPAKMLRKDLAIEFRLSAPRDLDLVLSKQYKVOIPGLENIQ 862
 QY 701 LSTLTLELCKGQAGELANGREILKAGSIGIGVD-----YVLNCLGNOTES 748
 DB 863 MFVPDYL---AEKSIILQDLNAAA---GKDCSKSDVDLIDAYLLITLTKHGRRARD 912
 QY 749 N-----NMQELGRLDLIRLLLEPAPFYPHIVSDVQGAEEVEYTRYKKLSTLFLAQ 803
 DB 913 SEDSKGTWEQO-----PVKVPVQVEYDILRSQVD-----NLLLVNQ 951
 QY 804 SIDNSHWGKLSRRIYLSARWVTV-----PAVFSKLEMLSVSSSTHTPRARRL 856
 DB 952 S---AHLTI---QRKAFQGISBGLMTLCOEQRTSSQVIAKALQQLK----- 991
 QY 857 MAIADVEIAEIQGVEDTLDGQDSFLQASVPNNYLETENSPECTVHLEKGT---- 912
 DB 992 ---NDALTELCNRISNAI--DRVHMFTESEFDAEVESESYTLQOYREAMIQGVNFCFEYH 1047
 QY 913 KGICATKLASSSDISERLASSISVGSSTTTTTTTTTEDQPKPVQVQTKGRPHSQCLNSPL 972

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Db 1048 KEYVRLMSGEFRKIDKXYSFARKMANYLTCESGRGRPRMATOGPFLOAIEPAFI 1107
Qy 973 SHHSQMLPFPALSTPSSSPSPAGTATDVSKHLOGFICRIPASAPOTGRKESLOFHRN 1032
Db 1108 SALPEDDFLSIALMNECIGHVIG-----KPH-----SPVT--GLYLAIHKN 1147
Qy 1033 CPENKSDLSIPYFQTSRPL-----PSSNIHRKP-----SRPRGNTSKOGDPSKN 1079
Db 1148 SP-----RPKVPKCHSDPKNPHLIIPFGFSTRKSPSARSHGSPAAA 1192
Qy 1080 SMTLDLNSSSKCDSPGSSNSNAVIPSDEVTFTPEEKCRLDVMTLNSIEDLLEAS 1139
Db 1193 AAAAAVAASRSPSG-----DSVLPKS-----ISSAHDTRGSS 1227
Qy 1140 MPSSDTFTVFKSEVAV-----LSPKAEKNDYK--DDVNHNOCKE--KMAAEDEAL 1189
Db 1228 VPENDRLASIAELQFRLSRHSPPTEERDEPAYPRKDSGSTRRSMELRTLISQKDTA 1287
Qy 1190 AIAAMASASODALPIYPQLOVENGEDIIIIQQ--DTPETLPG--HFKAKOPYREDTEWLK 1245
Db 1288 SKLPLFALQKSVRLFEEKKREMRKRNIIQVCDTPKSYDNVMHGLR--KVFETKMR 1344
Qy 1246 GOQIGLGAFFSSCYQADVGCTGLMAKOVYVYNTSSEGEVEVEALREIRKMSHLNHPN 1305
Db 1345 GKNTGSGQYGYKTYCTISVDTGELMAKEIFQPN----DHKTIKETRADELKITEGIRHPN 1400
Qy 1306 IIRMLGATCEKSNYLFIEEMAGGSVAHLISKYAFKESVINYTPQRLGLSYLHENOI 1365
Db 1401 LVYFVEVLHREEMVIFMEYCEDEGTLEE--VSRLG--LOEHVIRLYSKOYITAINVLEHGI 1458
Qy 1366 IHRDVGANLLIDSTGQRRLADFGAARLASG--TGAFQOQLGTFIAPAEVU--- 1421
Db 1459 VNHDDINGANIFLTSSG-LKLGDGCGSVKLKNAQTPMGCV--NSTLGTAAVMAPEVITRA 1516
Qy 1422 RGOQYGRSDVMSVGCALIEEMACAKPPMNAEKSHNLALFIKIASATTAPISFHSPLG 1481
Db 1517 KGGHGRADRWLGLGVIEIMYTGKRPWHYEYH--NFQIMYKGMG--HKRPPIERLSPEG 1573
Qy 1482 RDVALRCLELQPDPPRRELAKH 1505
Db 1574 KDFLSHLESDDPKMWTASQLDHD 1597

RESULT 13
H66221
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H66221
R:Phelodis, A.; Ecker, J.R.; Palm, C.D.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltz, R.; Marshall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakao, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southern, A.M.; Sun, H.; Tallon,
ker, M.; Wu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: H66221
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-652 <STO>
A:Cross-references: GB:AE005172; NID:g2342692; PIDN:AAB70419.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 6.2%; Score 484; DB 2; Length 652;
Best Local Similarity 37.3%; Pred. No. 3.1e-10;
Matches 113; Conservative 50; Mismatches 90; Indels 50; Gaps 10;
Qy 1228 PGHTAKOPYREDTEWLKGOQIGLGAFFSSCYQADVGCTGLMAKOVYVYNTSSEGEV 1287

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Db 57 PANTVDMAF---PISWKRGGLIGRAGFYVMGNMLDSGELLAKQVLIANAFAS--KEK 111
Qy 1288 VEALREIRRMNSHLNHNII-----RMGA-----TEKSN-----YNFIFEMA 1327
Db 112 TQLEEEVVKLLKNSHNIVVSNQCYLLNAGFNFSICLYLSNSVEDDTNLILEFV 171
Qy 1328 GGSVAHLISKYGAFFKESVINYTPQRLGLSYLHENOIHRDVGANLLIDSTGQRLRIA 1387
Db 172 GGSISLLEKFGPPPESEVRYTFQLLGLEYLHNHAIHRDIDGANILVDNNG--CIKLA 230
Qy 1388 DFGAANLASKGAGFQOQLGTFIAPAEVU--RGQYQ----- 1427
Db 231 DFGASKQVALALATWTG--AKSMKGTPLYMAPEVILQGHSPGDLCPIFLSHKPAVL 288
Qy 1428 RSDVMSVGCALIEEMACAKPPMNAEKSHNLALFIKIASATTAPISFHSPLGRVALR 1487
Db 289 SSADINWSGCTVIEIMYTGKAPMS--QQYKEVAALFFGTTKSHNPPIPTDILSSAKDPLK 346
Qy 1488 CLE 1490
Db 347 CLQ 349

RESULT 14
T51625
MAPK alpha protein kinase (EC 2.7.1.-) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 08-Sep-2000
C:Accession: T51625
R:Jouanin, S.; Hamal, A.; Lepoint, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y.
Gene 229, 171-81, 1999
A:Title: Characterisation of novel plant genes encoding MEKK/STK1 and Raf-related pr
A:Reference number: 224447; MUID:9916996; PMID:10095117
A:Accession: T51625
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-582 <JOU>
A:Cross-references: EMBL:AJ010090; PIDN:CAA08994.1
C:Genetics:
C:Keywords: phosphotransferase

Query Match 6.2%; Score 483; DB 2; Length 582;
Best Local Similarity 25.9%; Pred. No. 3e-10;
Matches 138; Conservative 84; Mismatches 166; Indels 144; Gaps 17;
Qy 1031 RNCPEKSDKLSVFTQSRPLFSSNIHRKPRPRPGNTSKOGDPSKNSMTLDLNSSSK 1090
Db 8 KSC-KNKD-DNHRGILISTDRDIXSAVVDP-PLTPRGGT-----PR 46
Qy 1091 CDDSPGSSNSNAVIPSDET-----VFTPV--EEKCRUDVNTLNSSTEDL---PR 1135
Db 47 CSREFAGASSAFSG-FPSDSTKKGHLPLRPLSPVSIHHQDHYSGSTSVSSVSS 105
Qy 1136 -----LEASMPSSDTFTVFKSEVAVLSPKAEKNDYTKDDVNHNOCKEKEAEDEE 1187
Db 106 GSADQSQALVASRQGD--VKFNVAAPRSPERSV----- 138
Qy 1188 AIAAMASASODALPIYPQLOVENGEDIIIIQODT-----PETLPGH 1230
Db 139 -----PKAATITTRTPSPHQRLSG--VVSLESSTRNDGRSSSECHLPREPPTS 190
Qy 1231 TKAKOPYRED-----TEMLKGOQIGLGAFFSSCYQADVGCTGLMAKOVYVYRNT 1280
Db 191 PSVHGRIRIGGYETSPSGSTWKKGFLSGTFQGYLTFGNSEKGMCAIKYKVIYSD 250
Qy 1281 SSGQEEVEVALREIRRMNSHLNHNIIIRMLGATCEKSNYLFIEEMAGGSVAHLISKYGA 1340
Db 251 QT-SKECLKQNLQDINLNLQCHPNIVQYGGSELSEETLSVLEYEVAGSGSIHKLKDYGS 309
Qy 1341 FKESVINYTPQRLGLSYLHENOIHRDVGANLLIDSTGQRLRIADFGAARLASKGT 1400

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Db	310	FTPEIQWTRRIILGLAVLHGRNTVHRIKGANILFK-----	347
OY	1401	GAGEFGQLLGIITAMPEVLRGQO-YGRGCVSVSCGAIITIMACAKKPPMNAEKHSNHL	1459
Db	348	-----SSPYMAAPEVVMSSQNGYTHAVDWIMSLGCTILLETAKTSKPPWS---QREGVA	394
OY	1460	LIFKIASATTAIPSPHSPLGRDVALKRLLEQPODRSPRELKHPVRRIT	1511
Db	395	ALFKGNSKDPIDELPDHLSNDAKNTIRLCLONNPVYRPASQCLLEHPPLRNT	446


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QY 236 VQASAAAPKGRSPSPGNSGRTYKSPGVRRKRVSVPVFGSGRTIPPRAPSPDG 235
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Db 231 GQGSAAAPKGRSPSPGNSGRTYKSPGVRRKRVSVPVFGSGRTIPPRAPSPDG 230
QY 296 FSPYSPEETNRNRYKMARLYLLOQIGPNSFLIGDSPNKKYRVETGPONSCARGTFC 355
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Db 291 FSPYSPEETNRNRYKMARLYLLOQIGPNSFLIGDSPNKKYRVETGPONSCARGTFC 350
QY 356 IHLFPMLRVFOLEPSDPMILMRKTLKNFEVESLFOKYHSRRSRIRKAPSNHTOKFVSRM 415
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Db 351 IHLFPMLRVFOLEPSDPMILMRKTLKNFEVESLFOKYHSRRSRIRKAPSNHTOKFVSRM 410
QY 416 SNHSTLSSSTSTSSSENSTKDEEOMCPICLLGMDEEVLTCCEGCRKRLHHHCSTW 415
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 411 SNHSTLSSSTSTSSSENSTKDEEOMCPICLLGMDEEVLTCCEGCRKRLHHHCSTW 410
QY 476 AEECRNRREPLICPLCRSKRSHDFYSHETLSPVDSPLRAAQOOTOQOPLAGS-RRN 534
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Db 471 AEECRNRREPLICPLCRSKRSHDFYSHETLSPVDSPLRAAQOOTOQOPLAGS-RRN 530
QY 535 QSNENFLHYGTQOIPRAYKDIAEPWIOVFGMELVGLFSRRNNVREMLRLSHDVSQA 594
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QY 595 LLLANGESTGNSGGSSGSGATSGSOTSTSGDVVEACCSVLNWCADPYKXYVVA 654
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Db 651 LKTLRAMLVYTPCHSLAERIKIOLRLQPVVDTLVNCADANSRTSOLSTLLELCKGA 710
QY 715 GELAVREILKAGSITIGVDYVLYNCLIGNQTSNNMOELGLCLIDRLLEFPAPFPY 774
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 711 GELAVREILKAGSITIGVDYVLYNCLIGNQTSNNMOELGLCLIDRLLEFPAPFPY 770
QY 775 HAYSTVSOAPEYRIKYLKLLSTLTFALOSIDNSHSMVGLSRITLSSARMTYPHVF 834
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Db 771 HAYSTVSOAPEYRIKYLKLLSTLTFALOSIDNSHSMVGLSRITLSSARMTYPHVF 830
QY 835 SKLEMLSVSSSTHTMRMRRLMAIADVEIAEAIQIADVEDTLDGQODSFLQASVPNLY 894
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Db 831 SKLYTMLNAGSSTHTMRMRRLMAIADVEIAEAIQIADVEDTLDGQODSFLQASVPNLY 889
QY 895 ETTENSPECTYVHLEKGTGGLCTKLSASSEDISERLASSVGPSSSTTTTTTQPKP 954
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Db 890 ---ENSSLHTYHREKGTGGLSATRLSASSEDISDRLAGVSGLPSS-----TTTQPKP 941
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Db 942 AYQTKRPHSOCISSPLSHHSQMLPALTPSSSTPVPAGTATVSKHRLGFTPCRT 995
QY 1015 PASAPQTKRFFSLQFHRNCPENKDKSLSPVFTQSRPLPSSNTHRPKPSHPTPGNTSKOG 1074
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QY 1075 DSKNSMTLDMSSSKCDSDSGSSNNAVTPSDVETVTPVBEKRLDVNTFLANSIED 1134
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Db 1056 DSKNSMTLDMSSSKCDSDSGSSNNAVTPSDVETVTPVBEKRLDVNTFLANSIED 1115
QY 1135 LLEASRPSDDTYTFKSEVAVLSPEKAENDDTKYDYNHNOCKEKEMAEKEEALIAAMA 1194
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QY 1195 MSASODALPIVPOLOVENEDIIIIQODTPETLPGHTKAKOPYREDTEMLKGOOIGLGA 1254
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Db 1236 SSCYQADVGTGTLMAVKQVTVYRNTSSQOEVEVEALREIRMSGLNHPNITRMIGATC 1295
QY 1315 EKSNTYLFTEMNAGGSVAHLLSKYGAFKESVYINTVEQLLRGLSYLHENOIIHRDVKAN 1374
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Db 1356 LLDSTGQRLRIDFGAAARLAKSGTGAGFEQOLGTLFMAPEVLRGOQYRSCDWS 1415
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RESULT 2
US-10-000-864-8
; Sequence 8, Application US/10000864
; Patent No. US20020146798A1
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: CPT-08SCPPC
; CURRENT APPLICATION NUMBER: US/10/000,864
; EARLIER FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: USSN 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: USSN 60/099,165
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1493
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-000-864-8

Query Match 88.3%; Score 6912.5; DB 12; Length 1493;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 1358; Conservative 47; Mismatches 82; Indels 31; Gaps 11;

QY 1 MAAAAGNRASSSGFPGARATSPEA---GGGGGALKASAPAA-AAGLREAGSGGERAD 56
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Db 61 WRRRHRYKRVSVLDELPLEQPLEFLAASPPCPTSPSPPADAAASNFQPAAGPPRG 120
QY 116 AASRGAAHLTESYAADSGASPPAAEPGEKRAAPAEPSPPAAPAGRENNKETLGLKH 175
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Db 121 AASRGAAHLTESYAADSGASPPAAEPGEKRAAPAEPSPPAAPAGRENNKETLGLKH 170
QY 176 MODRPEERMIREKTKATCPAMKHEWLERNRNRPVYVPIPKGSGSENNHIAASPEE 235
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Db 171 MODRPEERMIREKTKATCPAMKHEWLERNRNRPVYVPIPKGSGSENNHIAASPEE 230
QY 236 VQASAAAPKGRSPSPGNSGRTYKSPGVRRKRVSVPVFGSGRTIPPRAPSPDG 295
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Db 231 GQGSAAAPKGRSPSPGNSGRTYKSPGVRRKRVSVPVFGSGRTIPPRAPSPDG 290
QY 296 FSPYSPEETNRNRYKMARLYLLOQIGPNSFLIGDSPNKKYRVETGPONSCARGTFC 355
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Db 291 FSPYSPEETNRNRYKMARLYLLOQIGPNSFLIGDSPNKKYRVETGPONSCARGTFC 350
QY 356 IHLFPMLRVFOLEPSDPMILMRKTLKNFEVESLFOKYHSRRSRIRKAPSNHTOKFVSRM 415
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Db 351 IHLFWMLRNFVLEPSPDMLMRKTLKNEFVESLFOKYHRSRRSRIKAPSRNTIOKPFVSRM 410
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QY 535 QESNFMILHTGTOQIPPAYDIAEPMIQVGMELVCLFRRNMVRRMALRRLSHDVSQA 594
Db 531 QESNFMILHTGTOQIPPAYDIAEPMIQVGMELVCLFRRNMVRRMALRRLSHDVSQA 590
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QY 655 LKTLRAMLVTPCHSLAERIKLORLQPVVDIILVVCADANSRISQSLSTILELCKGOA 714
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QY 835 SKLEMLSVSSSTHFTMRRLMAIADVEILAEIQLGVEDLIDGQODSFLQASVPMNYL 894
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QY 895 ETTENSPECTVLEKGTGKICATKLASSEDISERLASISVGSPSSTTTTTTTTEQPKP 954
Db 890 ---ENSLFHTVIREKTGKLSATRLSASSEDISDRLAGSVGLPSS-----TTTEQPKP 941
QY 955 MVOTKGRPHSOCNSPFLSHHSQMLPALSTPSSSTPSPVAGTADVSKHRLQGFICRI 1014
Db 942 AVOTKGRPHSOCNSPFLSHHSQMLPALSTPSSSTPSPVAGTADVSKHRLQGFICRI 995
QY 1015 PMSAPQORFSTIOFHNCENKDKLSPVFQSRPLPSSNTHRPSPRPTPNTSKOG 1074
Db 996 PMSAPQORFSTIOFHNCENKDKLSPVFQSRPLPSSNTHRPSPRPTPNTSKOG 1055
QY 1075 DPKNSTMTLNLSSSKCDDDFGCGSSNNAVIPSDETVFPVEEKCLDVTELNSSIED 1134
Db 1056 DPKNSTMTLNLSSSKCDDDFGCGSSNNAVIPSDETVFPVEEKCLDVTELNSSIED 1115
QY 1135 LLEBASPSSDITVTFKSEVAVLSPKAEENDTYKDVNHNQCKEKKMAEKEEALATAMA 1194
Db 1116 LLEBASPSSDITVTFKSEVAVLSPKAEENDTYKDVNHNQCKEKKMAEKEEALATAMA 1175
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QY 1375 LLLDSTGQRIADFGAAALASKGTGAGEFOGLCTIAPMADEVLRGOQYGRSCVWS 1434
Db 1356 LLLDSTGQRIADFGAAALASKGTGAGEFOGLCTIAPMADEVLRGOQYGRSCVWS 1415
QY 1435 VGCATIEMACAKPPMNAEKSHNLALFKTASATTAISPSHSGRLDVALRCLLEPOQ 1494
Db 1416 VGCATIEMACAKPPMNAEKSHNLALFKTASATTAISPSHSGRLDVALRCLLEPOQ 1475

QY 1495 DRPPSREILKHPVETTW 1512
Db 1476 DRPPSREILKHPVETTW 1493
RESULT 3
US-09-858-754-4
; Sequence 4, Application US/09858754
; Patent No. US20020055130A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OR INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS
; FILE REFERENCE: CPl-042
; CURRENT APPLICATION NUMBER: US/09/858, 754
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/023,130
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/039,740
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1493
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-858-754-4

Query Match 88.1%; Score 6892.5; DB 10; Length 1493;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 1350; Conservative 45; Mismatches 96; Indels 23; Gaps 8;

QY 1 MAAAGNRASSGCFPGARATSPKAGGGGALKASAPAAAGLIREAGSGGERADWRR 60
Db 1 MAAAGNRASSGCFPGARATSPKAGGGGALKASAPAAAGLIREAGSGGERADWRR 60
QY 61 QLRKRVSYELDQLEPDLPLFLAAPPASTSPSPEDADAGSGTGFOYAVPPHGAASRG 120
Db 61 QLRKRVSYELDQLEPDLPLFLAAPPASTSPSPEDADAGSGTGFOYAVPPHGAASRG 120
QY 121 GAHITESVAAPDSCASSPAAAEPEKRAPAEPSPAAAPAGREMKETLGLHKMDRP 180
Db 121 GSHAEIATAADSGARSPAGAP-----PS-AAAPSGREMKETLGLHKMDRP 170
QY 181 EEMIRREKATCAMPAMKHEWLERRNRGPVYVPIPKGSGSEMNHIAESPEVQASA 240
Db 171 EEMIRREKATCAMPAMKHEWLERRNRGPVYVPIPKGSGSEMNHIAESPEVQASA 230
QY 241 ASPASKGRSPSPGNSDGRVKSSEPGVRRKRVSPVPFQSGRTTPPRRASPDSFSPYS 300
Db 231 AAPAPKGRSPSPGNSDGRVKSSEPGVRRKRVSPVPFQSGRTTPPRRASPDSFSPYS 290
QY 301 PEENRRNRKMYRRLYLQOIGPNSFLIGDSDPNKRYVITGPNCSGACGTCTIHLF 360
Db 291 PEENRRNRKMYRRLYLQOIGPNSFLIGDSDPNKRYVITGPNCSGACGTCTIHLF 350
QY 361 VMLRVFOLEPDPMLMRKTLKNEFVESLFOKYHSRRSRIKAPSRNTIOKPFVSRMNSHT 420
Db 351 VMLRVFOLEPDPMLMRKTLKNEFVESLFOKYHSRRSRIKAPSRNTIOKPFVSRMNSHT 410
QY 421 LSSSSTSTSSSENISKDEEOMCPICLLGMLDEESLTVCEDCRNLHHHCKSIWAEBCR 480
Db 411 LSSSSTSTSSSENISKDEEOMCPICLLGMLDEESLTVCEDCRNLHHHCKSIWAEBCR 470
QY 481 RNRREPLICPLCRSKRSHDFYSHELSSPYVDSPLRAAOQOVQOOLAGS -RRN 539
Db 471 RNRREPLICPLCRSKRSHDFYSHELSSPYVDSPLRAAOQOVQOOLAGS -RRN 530
QY 540 NLTHYGTQOIPPAKXDLAEPMIQVGMELVCLFSRMNVRRMALRRLSHDVSQALLAN 599
Db 531 NLTHYGTQOIPPAKXDLAEPMIQVGMELVCLFSRMNVRRMALRRLSHDVSQALLAN 590
QY 600 GESTGNSGSGSSPGSGATSSGTSISGDVVEACCSVLSMVCADPYKVVYAAALKTUR 659

591 GPGTSGGGSGGSLAGAGSSGSSPSISGDVYEAFCVSILYCADPYKVVYAAALKTLR 650
QY 660 AMLVYTPCHSLAERIKLQRLQPVDTILVKCADANSRTSQTSLSTLLELCCKGQAGELAV 719
DB 651 AMLVYTPCHSLAERIKLQRLQRPVDTILVKCADANSRTSQTSLSTLLELCCKGQAGELAV 710
QY 720 GREILLKAGSIGGVYVNCILGNOTESNNQELLGRCLDLRLLEPAEYPIHVST 779
DB 711 GREILLKAGSIGGVYVNCILGNOTESNNQELLGRCLDLRLLEPAEYPIHVST 770
QY 780 DYSQAEPEVIRKYLILSTLTFALQSDINSHMWGKLSRRYLSASRMVTPVPEFSKLE 839
DB 771 DYSQAEPEVIRKYLILSTLTFALQSDINSHMWGKLSRRYLSASRMVTPVPEFSKLT 830
QY 840 MLSVSSSTHTNRRRLMAIADEVEIAEAIQLGVEDTLDGQDSFLQASVPNNYLETTEN 899
DB 831 MLSAGSSSHFARMRRRLMAIADEVEIAEVIQLGSEDTLDGQDS--SQLAPPRY---PES 886
QY 900 SSPCTVHLEKTGKGLCAKRLSSSEDISERLASISVG--PSSSTTTTTTTTTEQPKMVOT 958
DB 887 SLEHTAHVEKTKGKGLKATRLSSSEDIDRLAGSVGLPSSA-----TTQPKPTVOT 940
QY 959 KGRPHSQCLNSSPLSHSOLMFPALSTPSSSTPVATADYKSHRLOGFICRIPSPAS 1018
DB 941 KGRPHSQCLNSSPLS--PQLMFPALSTPSSSTPVATADYKSHRLOGFICRIPSPAS 999
QY 1019 PGTQKRFSLQFHRNCPENKOSDKLSPVETQSRPLPSSNTHRPKSPRPTGNTSKQDPSK 1078
DB 1000 PGTQKRFSLQFHRNCPENKOSDKLSPVETQSRPLPSSNTHRPKSPRPTGNTSKQDPSK 1059
QY 1079 NMTLIDNSSKRCDSFGGSSNSNAVIPSDEVTFTVPEKGLDVTLELNSIEDLLER 1138
DB 1060 NMTLIDNSSKRCDSFGGSSNSNAVIPSDEVTFTVPEKGLDVTLELNSIEDLLER 1119
QY 1139 SMPSSDTVTTFKSEYAVLSPKAEKNDTYKDDVNNHQCCKEKEAESEALATAMASAS 1198
DB 1120 SMPSSDTVTTFKSEYAVLSPKAEKNDTYKDDVNNHQCCKEKEAESEALATAMASAS 1179
QY 1199 ODALPIVPOLOVENGEDIIIIIOODPPELTPGHTKAKOPYREDTMWLKGQOIGLAFSSCY 1258
DB 1180 ODALPIVPOLOVENGEDIIIIIOODPPELTPGHTKAKOPYREDTMWLKGQOIGLAFSSCY 1239
QY 1259 QADODGTGLMAVKQVTVYRNTSSQEEVEVALREIIRMSHNLNHNITRMGATEKSN 1318
DB 1240 QADODGTGLMAVKQVTVYRNTSSQEEVEVALREIIRMSHNLNHNITRMGATEKSN 1299
QY 1319 YMLFTEWMAAGSVAILSKYGAFFESVINTYEQLLRGSLYHENOIIHRDYGANLLID 1378
DB 1300 YMLFTEWMAAGSVAILSKYGAFFESVINTYEQLLRGSLYHENOIIHRDYGANLLID 1359
QY 1379 STGQRLRIADFGAARLASKGTGAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCA 1438
DB 1360 STGQRLRIADFGAARLASKGTGAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCA 1419
QY 1439 IIEWCAKPRMAEKHSNHLALIFKIASATTPASIPSHLSPGLRDVALKCLEIQDQDRP 1498
DB 1420 IIEWCAKPRMAEKHSNHLALIFKIASATTPASIPSHLSPGLRDVALKCLEIQDQDRP 1479
QY 1499 SRELLKHPVETTW 1512
DB 1480 SRELLKHPVETTW 1493

CURRENT APPLICATION NUMBER: US/10/000,864
; CURRENT FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: USSN 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: USSN 60/099,165
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-864-2
Query Match 80.7%; Score 6318.5; DB 12; Length 1302;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 1230; Conservative 26; Mismatches 46; Indels 15; Gaps 5;
QY 196 AMKHEMLERNRRGPPVYKPIPKGDSSENNHLAESPGEVQASASPASKGRSPGPN 225
DB 1 AMKHEMLERNRRGPPVYKPIPKGDSSENNHLAESPGEVQASASPASKGRSPGPN 60
QY 256 SPGRTVKSSEPGVRRKRVSPVPFGSGRTIPPRAPSPDGFSPSPETRRRVKRVAR 315
DB 61 SPGRTVKSSEPGVRRKRVSPVPFGSGRTIPPRAPSPDGFSPSPETRRRVKRVAR 120
QY 316 LYLQOIGRPSFLIGDSDPNKTRVITGPONCSANGTFCIHLLFYMLRVFOLEPSDPL 375
DB 121 LYLQOIGRPSFLIGDSDPNKTRVITGPONCSANGTFCIHLLFYMLRVFOLEPSDPL 180
QY 376 WRKTLNFEVESLFQKYHSRSSRIKAPSNRTQKQVSRMSNHTLSSSTSSSENST 435
DB 181 WRKTLNFEVESLFQKYHSRSSRIKAPSNRTQKQVSRMSNHTLSSSTSSSENST 240
QY 436 KDEEQMCPICLLGMLDESLTVCEDCRNKLHHNCSIMAEBCRRNRREPLICPLCRSKW 495
DB 241 KDEEQMCPICLLGMLDESLTVCEDCRNKLHHNCSIMAEBCRRNRREPLICPLCRSKW 300
QY 496 RSHDFTSHLSFVDSPTSIRAAQOQTVQOPLAGSRNDSFNLTHTGTQOIPPAYKD 555
DB 301 RSHDFTSHLSFVDSPTSIRAAQOQTVQOPLAGSRNDSFNLTHTGTQOIPPAYKD 360
QY 556 LAEPWIOVGMELVGLFESNNMVRMALRRLSHDVSGALLANGSTGSSGSSSPS 615
DB 361 LAEPWIOVGMELVGLFESNNMVRMALRRLSHDVSGALLANGSTGSSGSSSPS 420
QY 616 GCATSGSSQTSISGDVVEACCSVLSMWCADPYKVVYVAALKTLRAMLVYTPCHSLAERIK 675
DB 421 AGAAGSSQPSISGDVVEACCSVLSMWCADPYKVVYVAALKTLRAMLVYTPCHSLAERIK 480
QY 676 IQRLQPVVDTILVKCADANSRTSQTSLSTLLELCCKGQAGELAVREILLKAGSIGGVYD 735
DB 481 IQRLQPVVDTILVKCADANSRTSQTSLSTLLELCCKGQAGELAVREILLKAGSIGGVYD 540
QY 736 YVNCILGNOTESNNQELLGRCLDLRLLEPAEYPIHVSTVDSQAEPEVIRKYL 795
DB 541 YVNCILGNOTESNNQELLGRCLDLRLLEPAEYPIHVSTVDSQAEPEVIRKYL 600
QY 796 SLTTFALQSDINSHMWGKLSRRYLSASRMVTPVPEFSKLEMLSVSSSTHTNRRRL 855
DB 601 SLTTFALQSDINSHMWGKLSRRYLSASRMVTPVPEFSKLEMLSVSSSTHTNRRRL 660
QY 856 LMAIADEVEIAEVIQLGVEDTLDGQDSFLQASVPNNYLETTENSSPECTVHLEKTGKL 915
DB 661 LMAIADEVEIAEVIQLGVEDTLDGQDS--LQALAPASCL---ENSLERTVHREKTKGKL 716
QY 916 CATKLSASEDISERLASISVGPSSSTTTTTTTTTEQPKMVOTKGRPHSQCLNSSPLSH 975
DB 717 SATRLSASEDISERLASISVGPSS-----TTTEQPKMVOTKGRPHSQCLNSSPLSH-H 770

RESULT 4
US-10-000-864-2
; Sequence 2, Application US/10000864
; Patent No. US20020146798A1
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
; FILE REFERENCE: CPT-085CPC

QY	976	SOFFPLSTSPSSSTPEVACGTIDVSKIRLQGIPICRIPSAPOCKRFSQIFHRNCE	1033
Db	771	AQLMEPPASACSSABVP-----DISKHPQAFVPCKIPASPOTKRFSQIFHRNCE	825
QY	1036	NKQSDKLSPEFTQSRPLPSSNIHRPPPSRPTGQNTSKQDPKNSMTLIDLNSSKCDQSF	1095
Db	826	HRSDQLSPVFTQSRPPSSNIHRPPPSRPTGQNTSKLGDATKSSMTLIDLSASCDDSF	885
QY	1096	GCSSNSSNAVIPDEYVFTYVEKCRJLDVTELNSSITEDLLEASMPSSDTVTYKSEYAV	1155
Db	886	GGGSGNSNAVIPSDEYVFTYVEKCRJLDVTELNSSITEDLLEASMPSSDTVTYKSEYAV	945
QY	1156	LSPKAKNDPTTKQDVVHNOCKEKEKEAEPEALATAMASASODALPIVPOLOVENED	1215
Db	946	LSPKAKNDPTTKQDVVHNOCKEKEKEAEPEALATAMASASODALPIVPOLOVENED	1005
QY	1216	IIIIIOOQPTPLPGHTKAKQPYREDTEWMLKGOQIGLGAESSCYQADVGSTGLTAAVKQT	1275
Db	1006	IIIIIOOQPTPLPGHTKAKQPYREDTEWMLKGOQIGLGAESSCYQADVGSTGLTAAVKQT	1065
QY	1276	YVRNTSSQEEVVEALREELIRMSHSHNHPRIIRMGATCEKSNYLIETEMAGGSVALLL	1335
Db	1066	YVRNTSSQEEVVEALREELIRMSHSHNHPRIIRMGATCEKSNYLIETEMAGGSVALLL	1125
QY	1336	SKYGAFFESVYINTTEQLLGLSYLHENQIIRHDVYGAMLLIDSTGQRLIADFEQAARL	1395
Db	1126	SKYGAFFESVYINTTEQLLGLSYLHENQIIRHDVYGAMLLIDSTGQRLIADFEQAARL	1185
QY	1396	ASKGTGAGEEQQLGLTIAMAEVYLRCGOYGRSCVWSYGCALITBMACAPMAEKHS	1455
Db	1186	ASKGTGAGEEQQLGLTIAMAEVYLRCGOYGRSCVWSYGCALITBMACAPMAEKHS	1245
QY	1456	NHMLLIRKIASATAPISPIHSLSPGLRDVALRCLTELQPDPRPSRELLKHPFRITTW	1512
Db	1246	NHMLLIRKIASATAPISPIHSLSPGLRDVALRCLTELQPDPRPSRELLKHPFRITTW	1302
RESULT 5			
US-09-858-754-5			
Sequence 5, Application US/09858754			
Patent No. US20020055130A1			
GENERAL INFORMATION:			
APPLICANT: Johnson, Gary L.			
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS			
FILE REFERENCE: CPI-042			
CURRENT APPLICATION NUMBER: US/09/858,754			
CURRENT FILING DATE: 2001-05-16			
PRIOR APPLICATION NUMBER: 09/023,130			
PRIOR FILING DATE: 1998-02-13			
PRIOR APPLICATION NUMBER: 60/039,740			
PRIOR FILING DATE: 1997-02-14			
NUMBER OF SEQ ID NOS: 13			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 5			
LENGTH: 1034			
TYPE: PRT			
ORGANISM: Homo sapiens			
FEATURE:			
OTHER INFORMATION: Xaa's at positions			
OTHER INFORMATION: 19,20,30,52-55,57,58,60,61,68,159,164,174-305,336,			
OTHER INFORMATION: 339,341,344,351,352,355,375,519,555,556,601,692,69			
OTHER INFORMATION: 5-739,767,769,777-814,819,827,834,862,864,870,875,			
OTHER INFORMATION: and 890 may be any amino acid			
OTHER INFORMATION: Xaa's at positions 901,904,916,922,932,943,946,			
OTHER INFORMATION: and 1034 may be any amino acid			
US-09-858-754-5			

Query Match	40.9%	Score 3200	DB 10	Length 1034
Best Local Similarity	64.3%	Pred. No. 3.8e162		
Matches 677; Conservative	25;	Mismatches 325;	Indels 26;	Gaps 9;

QY 465 NKLHHCMSIWAEECRNRREPLICPLCRSKWRSHDFYSHELLSPVDSPPSLRAAQQQTVO 524

Db	1	NKLHHOMSLIAEBCRRNXXPLICLCRSXMSHDFYSHELSSPDPSSLSLXXXXQXXVX	60
QY	525	QOPLAGS-RRNOSNENLHYGTQOIPPAYKDLAEPIOVFMELVGLFSRNNVREMA	583
Db	61	XHPLAGSXRRNOESNFMJTYGTQOIPPAYKDLAEPIOVFMELVGLCFRNNVREMA	120
QY	584	LRLSHVSGALLLANEESRNGSGSSGSPSGGATSSGSSISGDIIVENACSVLSMYC	643
Db	121	LRLSHVSGALLLANEESRNGSGSSGSPSGGATSSGSSISGDIIVENACSVLSMYC	180
QY	644	ADPYKYVAALKTLRAMLVYTPCHSLAEIRIKLQRLQPVDTIIVKCADANSRFSQISI	703
Db	181	XX	240
QY	704	STLELCGAGELANGREILKAGSIGIGVDYVILCJLGNOTESNMOELLGRCLIDR	763
Db	241	XX	300
QY	764	LLEPFAPEFYPHVSPVDSQAEPELRYKKLSLTLFALQSIDNSHWSVGLSLR---I	819
Db	301	XXXXXXXXPEFYPHVSPVDSQAEPELRYKKLSLTLFALKXIDSHWSGXSKRDISL	360
QY	820	YLSARAVTTPVPHVSKLEMLSVSSSTFTRRRLRLMAIDEEVIAIAIOLUGEDTLDG	879
Db	361	CYDDGRANVCF---SMXCMILSLSTHFTRRRLRLMAIDEEVIAIAIOLUGEDTLDG	416
QY	880	QOOSFLOASVPNNYLETTENSPECTVHLKTKGKLCATKLSASSEDISERIASVQ-P	938
Db	417	HQDS-LRALAP---ASCRENSELEHYHREKTKGLSATRLSTSEEISDRLAGSVGFP	472
QY	939	SSSTTTTTTEQRPVWQYKGGPHQCNSSPSLSHQSOLMPALSTSSSTPSVPACTA	998
Db	473	SS---TTTEQRPVWQYKGGPHQCNSSPSLS-HAQMPASVACSAPVYP---521	521
QY	999	TDVSKHRLQGIPIRIPASAPOTQRFKSLQFHNCENSDPSKLSPVYFOSAPLSSNIH	1058
Db	522	-DISKHPQAFVPEKILPHLPOTQRFKSLQFHNCENSDPSKLSPVYFOSAPLSSNIH	580
QY	1059	RPKRSPRTPGNTSKQGDPSKNSMTLJLNSSSKCDSDFCGSSNSSNAVIPSEVTFPYEE	1118
Db	581	RPKRDPAPGSGSTKLGATKSSMTLJLQGCRCDSDFGGGSGSNAAVIPSEVTFPYED	640
QY	1119	KCRLDVMTLNSSTIEDLLESMSPSDTYTFKSEVAVLSEPAENDDTYKDYVHNQCK	1178
Db	641	KCRLDVMTLNSSTIEDLLESMSPSDTYTFKSEVAVLSEPAENDDTYKDYVHNQCK	700
QY	1179	EKMEAEBEELAIAMASQDALPIVPOUYENGBDIIIOODPPELTPGHTRAKOPYR	1238
Db	701	XX	760
QY	1239	EDTEMLKGOOIGLGAFFSCYOADVGITGLMAVQYTVVRNNTSSBOEEVVALREELRM	1298
Db	761	EDAEMLKGOOIGLGHFFXXEETXM	820
QY	1299	SHLHNPMTIRMLGATCKRSNYNLFETMAGGSVAHLSTYGFKFSYVINTEDLRLGLS	1358
Db	821	SHLHNPMTIRMLGATCKRSNYNLFETMAGGSVAHLSTYGFKFSYVINTEDLRLGLS	880
QY	1359	YLHENQJIIHRVKGANLLIDSTGORLIDDFGAARLASKGAEPGOLGLGTAFAP	1418
Db	881	YLHENQJIIHRVKGANLLIDSTGORLIDDFGAARLASKGAEPGOLGLGTAFAP	940
QY	1419	EVLKGOOYGRSCDWSVGCAIEMACAPPMNAEKSHNLALFKIASATTAPISPHLS	1478
Db	941	EVLKGOOYGRSCDWSVGCAIEMACAPPMNAEKSHNLALFKIASATTAPISPHLS	1000
QY	1479	PGLRDVALRCLLEQPODRPSPRELKHPYFRTT1511	
Db	1001	PGLRDVALRCLLEQPODRPSPRELKHPYFRTT1033	

RESULT 6

US-09-858-754-2
Sequence 2, Application US/09858754
Patent No. US2002005130A1
GENERAL INFORMATION:
APPLICANT: Johnson, Gary L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS
FILE REFERENCE: CPT-042
CURRENT APPLICATION NUMBER: US/09/858,754
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/023,130
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/039,740
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 672
TYPE: PRT
ORGANISM: Homo sapiens
US-09-858-754-2

Query Match 39.6%; Score 3102.5; DB 10; Length 672;
Best Local Similarity 89.2%; Pred. No. 3.2e-157;
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY 826 MYTTPHVFESKLEMLSSSTHTRMRRLMAIDVEIAIQLGVEDTLDGQDSFL 885
DB 1 MYTAPAVFESKLEMLSSSTHTRMRRLMAIDVEIAIQLGVEDTLDGQDSFL 59
QY 886 QASVNNYLETENSSPECTVHLEKTKGLCATKLSSASESISERLASTSPSSSTTTT 945
DB 60 QAVAFESKLEMLSSSTHTRMRRLMAIDVEIAIQLGVEDTLDGQDSFL 112
QY 946 TTTTQPKPVMQTKGRPHSQCLNSPLSHSQMLPAPALSTPSSSTPSPAGTATDVSKHR 1005
DB 113 TTTTQPKPVMQTKGRPHSQCLNSPLSHSQMLPAPALSTPSSSTPSPAGTATDVSKHR 165
QY 1006 LOGFPCILPSPASPTQKRFSLQFHRNCPENKDSKLSVFFQSRPLPSSNTHRRKPSRP 1065
DB 166 POAFVPCILPSPASPTQKRFSLQFHRNCPENKDSKLSVFFQSRPLPSSNTHRRKPSRP 225
QY 1066 TPGNTSKQDPSKNSMTLDLNSKCDSDFGCSNSNSNIVSDETVFVEEKCRLDN 1125
DB 226 VPGSTSKGLDARKSSMTLDLGSASKCDSDFGCSNSNSNIVSDETVFVEEKCRLDN 285
QY 1126 TELNSSIEDLEASMPSSDPTVTFKSEVAVLSPEKAENDTYKDDVNHQCKEKEAE 1185
DB 286 TELNSSIEDLEASMPSSDPTVTFKSEVAVLSPEKAENDTYKDDVNHQCKEKEAE 345
QY 1186 BEALIAAMMSASDALPIVQLOVENGEDIIIOODTPETLPHTKAKQPTREDEWK 1245
DB 346 BEALIAAMMSASDALPIVQLOVENGEDIIIOODTPETLPHTKAKQPTREDEWK 405
QY 1246 GOQILGAFSSCYQADVGTGLMAVKQTYVYRNTSSEOEVEYEAALREIRMSHLNHN 1305
DB 406 GOQILGAFSSCYQADVGTGLMAVKQTYVYRNTSSEOEVEYEAALREIRMSHLNHN 465
QY 1306 IIRMLGATCEKSNYMLFTEWMAGGSVAHLISKYGAFFKESVINTYEQLLRGLSTLHENO 1365
DB 466 IIRMLGATCEKSNYMLFTEWMAGGSVAHLISKYGAFFKESVINTYEQLLRGLSTLHENO 525
QY 1366 IHRDVKANLLDSTGQRLRIDFGAARLASKGTGAGFGQQLGTFMFAPEVLRGO 1425
DB 526 IHRDVKANLLDSTGQRLRIDFGAARLASKGTGAGFGQQLGTFMFAPEVLRGO 585
QY 1426 YGRSCDVMSVGCATTEMCAKPPMAEKSHNLALIFKASATTAPSIPSHLSPGLRDA 1485
DB 586 YGRSCDVMSVGCATTEMCAKPPMAEKSHNLALIFKASATTAPSIPSHLSPGLRDA 645
QY 1486 LRCELQPODRPPRELLKHPVFRFTTW 1512
DB 646 VRCELQPODRPPRELLKHPVFRFTTW 672

RESULT 7
US-09-801-368-52
Sequence 52, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 52
LENGTH: 1478
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-52

Query Match 7.9%; Score 619; DB 10; Length 1478;
Best Local Similarity 21.0%; Pred. No. 3.2e-25;
Matches 332; Conservative 232; Mismatches 532; Indels 466; Gaps 64;

QY 224 ENNHLEASPEGEQASAPASPKGR-----RSPSPG---NSPSGRVKSSEPGVRRR 273
DB 24 KGHQHTSSVAVATKSSKSPRATSRKSIYODIRSGFNPILNPTSSQFYES----- 74
QY 274 VSPVFPQSRITPPRPAAPDGEPSYSPETNRVKKVNRARLYLQOIGPNSFLIGDS 333
DB 75 -TPVIEQSPFNWT-----TDDHISACTLE-----NPTSTNSSYK 107
QY 334 PNKYVVFVIGPONSCAR---GTFCHLFLVMLRVQLEPSPMLM---RKT----- 379
DB 108 NDN-----GPSLSDSKRSGGNSVNSLFDKLIISMDPTDDEMTMIRVTSWEKHFDF 161
QY 380 -----LNFEVESLFORYHSRRSRIRAPSRNTIOKEVSR-MSNS 418
DB 162 PESWILFFKQHLEFGRFKLLAYDNFAVEYKLPQTKTASTYRFOQLKMTKNTVNS 221
QY 419 H-----TLSSSTYSTSSSENSIKDEEOMCPICLGLMDESLTYCEDG-----RKK 466
DB 222 HIRKASAKLSRSSSESISIKLKNKSOE--DISNRSSTESALSPTKSPSTDEKMF 280
QY 467 LHHHCMSIAEECRNRREPLICPLCRSKWRSHPVSHELSSPVDSPSSIRAAQOQVVOO 526
DB 281 LH-----STSHOKTYSASSLYTRSFISLKGSSSNVASSAKSPSNIKL-----SIPAR 328
QY 527 PLAGSRNDESNFNLTHVYTOQIIPRAYKDLAEPIWQFEMELVGLFSNNMVREMAR 586
DB 329 P-----HSIENSSTLTKASPPASPEYPS-----IFRHH-----HK 360
QY 587 LSHDVSGALLLANGESTGNSGSSGSSPSGATSGSS-----QTSISDVYACCS 637
DB 361 SSSSESLINSLFGSGIGEAFTK--PNPQGHSLSENLAKGSKHYETVNSPLKGS--- 416
QY 638 VLSMCADPVYVYVAALTLTIRAMLVYTTCHSLAEIKIKRLQVVDVITLYKCADANSR 697

Db 417 --SLPTSDKGNLM--NKFRRSQICVPSNPVAVYTSQ-----ETPSLK----SNSS 461
 QY 698 TSQLSISTL-----LELCQAGELAVGREILKAGSIGGVADVYVNLCLGN 744
 Db 462 TATLTQTAADVNIIPSSSSPPPIKPTANRSLVSTEDTETSTASFKETYPDCINPD 521
 QY 745 QT---ESNNMOELLGRCLLDRLLEPPAFYHIYSTDVSOAE-----PV 787
 Db 522 KTVVPVANN--OKYSVKNFELDQ-----KFYP-LKRTGLDENSEKYLVTKDNVSEVPL 572
 QY 788 EIR-YKLLSLTFLFALQSDINSHSMV-----GK 814
 Db 573 NLSVAKLSFKESALTKLILNKNVTFFHMTDPCDIOGAILPDOTLEFLKSLFLNTSGK 632
 QY 815 LSRRIYLSARWYTPVPHVSKLEMLSVSSSTHFTMRRLMAIADEVEIAEAIQ--LG 872
 Db 633 IYIKDQKLIQKRPAPLVTENNVPILKSVKSSMRSGTSLASTDVSIVTSSDITS 692
 QY 873 VEDTLGQODSFTQASVPNNYLETENSSP-----ECYHLEKTKGKLCAT--KL 920
 Db 693 FDBHASSGGRRYPO--TPSYYYDRVSNTPTEELNWNIREVLSHERNAPRMVFKTSPKL 750
 QY 921 SASSEDSERLASISVGSSTTTTTTQPKPMVOTKGRPHSQCLNSS-----PLSHH 975
 Db 751 ELNLPKGSKL-----NIPPIITENESSKFQYLKDEGTIDFNHR 792
 QY 976 SOLMF--PALSTPSSSPVAPAGTADVSKHRLQGFIPCRIPASPOTORKFSLOFHRNC 1033
 Db 793 RESPYRPELA--PKREAPKRPAMTSPQRTLSTSKONKIRLVASTYISRS-----842
 QY 1034 PEKSDOKLSPVTTQSPPLPSSNHRP--KPSRPPTGNTSKOGDPSKSMVL-----D 1084
 Db 843 -----KRSKPLPOLSLSPLEASSSSPSDLTSSYPASTHVLIPQYKAND 889
 QY 1085 LNSSSKCD--DSFGSS-----NSNAVIPSEVTF--TP-----VEEKRL 1122
 Db 890 VMARLKTQDSTSTSPSLKAKOKYVNSNIVSTNSIFYSPLKLKGNKRYVSTISAA 949
 QY 1123 DVNTELNSSIEDLLEASMP-----SSDTVTYRKSEVAV-----LSPKAEV 1163
 Db 950 DIFEE--NDITFADAPMPFDSDDDDSSDDIIMSKKAPETNNENKDKEDSDN 1004
 QY 1164 DDTYKDVNNOKCKEME-----AEEELALAMASASODA 1201
 Db 1005 SSTHSDEIFYDSQODMERKMTFRPSPEVYVONLEKFFPRANIDKPIITEGIASPTSPKS 1064
 QY 1202 L-----PIVQLOVE-----NGEDIIIIQODTP-----1224
 Db 1065 LDSLISLKNVASSRTEPSTSPRPVPPDSSTYEFIODGLNGKKPLNOKAKTPKRTKTITIA 1124
 QY 1225 -----ETLPQH--TRAKOPYREDE--WLKGOQIOLG 1252
 Db 1125 HEASLARKNSVKLRONTKMGTRMVEVTENHMYINKAKNSKEVEFAMKEMKIGK 1184
 QY 1253 AFSSCYAODYGTGLMAVQVYVNTSSQOEYV--VEALREILMASHLNPNIIRM 1309
 Db 1185 SFGAVYICLVWTTGEMNAVQVE--VPKSSQNEALISTVEALRESEVSLKDLIDLHINTVOY 1243
 QY 1310 LGATCEKSNLNFIFEMWAGSVAHLLSKYGAFKESVIVNTEOLLRGISYHENQIIHRD 1369
 Db 1244 LGFENKNNTISLPLEYVAGSSVGLIMRYGFDEPLIKHLLTQVGLATYHSGILHRD 1303
 QY 1370 VKGANLLIDSTGQRLRIADFGAARLASKGTGAGEFOGOLLGTITAFMAPEVLRGOQY 1427
 Db 1304 MKADNLLDQDG--ICKISDPISRK--SKDIYSNS--DMTNGYVFWMAPEWVDVKOGISA 1359
 QY 1429 SCQVWSYGCAIIEMACAKPPMNAEKHSNHLALFKIASATTAPISPSHLSGLDVALR 1487
 Db 1360 KVDIWSYGCTVLEMFACKRPMS--NLEVYVAMFKIGKSKSAPPIDETPLPLISQIGRNF 1416
 QY 1488 ---CLELOPDRPSPRELKHP 1506
 Db 1417 LDACFEINPEKRPYANELLISHP 1438

RESULT 8
 US-10-000-864-12
 ; Sequence 12, Application US/10000864
 ; Patent No. US20020146798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
 ; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; FILE REFERENCE: CPI-085CPC
 ; CURRENT APPLICATION NUMBER: US/10/000,864
 ; CURRENT FILING DATE: 2001-10-31
 ; EARLIER APPLICATION NUMBER: 09/423,890
 ; EARLIER FILING DATE: 2000-06-03
 ; EARLIER APPLICATION NUMBER: PCT/US99/05556
 ; EARLIER FILING DATE: 1999-03-15
 ; EARLIER APPLICATION NUMBER: USSN 60/078,153
 ; EARLIER FILING DATE: 1998-03-16
 ; EARLIER APPLICATION NUMBER: USSN 60/099,165
 ; EARLIER FILING DATE: 1998-09-04
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 626
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-000-864-12

Query Match 7.1%; Score 559; DB 12; Length 626;
 Best Local Similarity 29.9%; Pred. No. 1.0e-22;
 Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOTQKRFSLQFHRNCPEKSDOKLSPVTTQSPPLPSSN-----IHRKP-----1062
 Db 110 SSMKSLRIILLSDDRN--HTSSPHSGVSRQYRIKPSQAGDINTIYQAPPRSRRLS 166
 QY 1063 -----SRPTPG-----NTSKQDPSKNSMTIDLNSSKCDDSFGCSSNSNAVIP 1107
 Db 167 VSSQNPGRSSPPGPVYPERQOHIARQ-----SYT-----SINSEGETP 206
 QY 1108 SDEIVTFVVEKCKLDVNTELNSSIEDLLEASMSSTDTYTFKSEVAVLP-----1158
 Db 207 E-----TSQCMIDLPSAENSLSGSCQSLDRSADSPSFRKQMSVARSFPDNRKES 259
 QY 1159 -----EKAENDPY-----KDVNHNOKCKEMEAEELALAI--AMASASQ 1199
 Db 260 DRETQIDKVGKGTTPRRIRYVSHHKDYNDGKRTPFIRRHQGNLTFLVSSSLSLNG 319
 QY 1200 DALPITVPQ-----LOVENGEDIIIIQODTPETLPHTKAKOPYREDTEWLKGOQIOLG 1252
 Db 320 ENMGVAOYLDPGRRLRSADSENALVQERNVPT-----KSP-SAPINMRCKLLGOG 371
 QY 1253 AFSSCYAODYGTGLMAVQVYVNTSSQOEYV--VEALREILMASHLNPNIIRM 1312
 Db 372 AFGVYICLVWTTGEMNAVQVE--VPKSSQNEALISTVEALRESEVSLKDLIDLHINTVOY 1243
 QY 1313 TCEKSN--YNFIFEMWAGSVAHLLSKYGAFKESVIVNTEOLLRGISYHENQIIHRD 1370
 Db 431 LRDNAEKLTITFMEYMGGSVKQDLKAYGALTESYTRKTYTQILEGMSYLSNMTIHRD 490
 QY 1371 KGANLLIDSTGQRLRIADFGAARLAS--KGTGAGEFOGOLLGTITAFMAPEVLRGOQY 1427
 Db 491 KGANILRDSAG--NVKLDFGASKRLQITICMSGTGI--RSVTGTPYVMSPEVLSGEGYG 545
 QY 1428 RSCQVWSYGCAIIEMACAKPPMNAEKHSNHLALFKIASATTAPISPSHLSGLDVALR 1487
 Db 546 RKADVWSYGCTVLEMFACKRPMS--NLEVYVAMFKIGKSKSAPPIDETPLPLISQIGRNF 1416
 QY 1488 CLELOPDRPSPRELKHP 1506
 Db 602 RIFVBARORPSAEELTH 619


```

QY      1417  APELNRQOQYGRCDVWSVCAICIAEMAAKCPMNMKEKSHNHALIFELKIASATAPISPS 1476
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      535   SPEVISEGEGGRADVWSLGGCTVVDMLTEKPPW-AEYEA--WAALFKIATQPTNQLPSH 591
QY      1477  LSPGLRDVALRCLELDQRPDRPPEKILLKH 1505
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      592  ISEHGGRDF-LRRIFVEAKRQPSAEELLTH 619

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RESULT 13
US-10-000-864-10

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?  GENERATED INFORMATION:
?  APPLICANT: CADUS PHARMACEUTICAL CORPORATION
?  TITLE OF INVENTION: HUMAN MEK1 PROTEIN AND NUCLEIC ACID MOLECULES
?  TITLE OF INVENTION: AND USES THEREFOR
?  FILE REFERENCE: CPT-085CPC
?  CURRENT APPLICATION NUMBER: US/10/000,864
?  CURRENT FILING DATE: 2001-10-31
?  EARLIER APPLICATION NUMBER: 09/423,890
?  EARLIER FILING DATE: 2000-06-03
?  EARLIER APPLICATION NUMBER: PCT/US99/05556
?  EARLIER FILING DATE: 1999-03-15
?  EARLIER APPLICATION NUMBER: USSN 60/078,153
?  EARLIER FILING DATE: 1998-03-16
?  EARLIER APPLICATION NUMBER: USSN 60/099,165
?  EARLIER FILING DATE: 1998-09-04
?  NUMBER OF SEQ. ID NOS.: 38
?  SOFTWARE: PatentIn Ver. 2.0
?  SEQ. ID NO. 10
?  LENGTH: 619
?  TYPE: PRT
?  ORGANISM: Mus musculus
?  IS-10-000-864-10

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Query Match 6.88; Score 531; DB 12; Length 619;
 Best Local Similarity 28.48; Pred. No. 4.8e-21;
 Matches 168; Conservative 214; Indels 132; Gaps 24;

QY	944	TTTTTTCOPMPYQOTGRPHSCLINSSPSHHSSOLMFALPSTPSSSTPSPVAGTATDVK	1003
Db	124	STQATNLEPSPSED-----LNTPTLGAERKRRLSVGCPNDRSSPPPGTLPDLH	175
QY	1004	H--RLOGTICR-----IPASPTQGRKESLQFHRNCPENKDSKLSBVTQSRPLPSN	1056
Db	176	QIARNGSFSTINSEGEFTIPESMDMDPLSTL-----SPENSGSGSCPSTL-----DSPLODES	228
QY	1057	IHRKPSRPRPGMTSKQGPBKSMTHLDMSSSKCDSDSCSS-----NS	1101
Db	229	Y--PKSMP-----RAQSTPDNHQFTD--NPJFEKGGKGTYPRRYHVSYHMQEYND	279
QY	1102	SNAVISDETVTPVEEKRCLDVNTFELNMSIEDLLEASMPSSDTPVTEKSEVAVLSPEKA	1161
Db	280	GRTKTF-----RARQTGTSFRSPV-----SPSPDHSLSHSSGSSVTPTE--	320
QY	1162	ENDTYKDDYNNHQKCKEKEHEEELALIMAMASQDALPIYQLOVENGEDITITIQ	1221
Db	321	-----YDSRIRRR-----GSDI-----	333
QY	1222	DPEE-TLPGHTKAKOPYREDTEWLKGOQIGLGAFFSCYOADVGCTLMAKQOVTYVNT	1280
Db	334	DNPTLYTDSPPRSRPRAPTNNRKLKLLGQAGAFGAVIYCTYVDGTRELAKQOYF-NPE	392
QY	1281	SSQOEVEVALREELIRMMSHLNHPNIIIMLGATC-----EKSYNLFTEMMAGSVAILLS	1336
Db	393	SPESKSEVNALCEIOILLNLNLHERIVQYGG--CARDPEKTLSTFEMELSPGSGSTKDQK	450
QY	1337	KYGAFKESVYINTTEOLLGLSTJHENOIHHVDYGANLLIDSTQGRLLRINDEFGAAATA	1396
Db	451	AYGALNENTRKRTROLLECVAHLSNMIVHDIDIGANLIRDSTG--NKLKDPFGASKRLQ	509

[illegible]

RESULT 14
US-10-000-864-4
; Sequence 4, Application US/10000864

```

? APPLICANT: CAODS PHARMACEUTICAL CORPORATION
? TITLE OF INVENTION: HUMAN MEK1 PROTEIN AND NUCLEIC ACID MOLECULES
? TITLE OF INVENTION: AND USES THEREFOR
? FILE REFERENCE: CPT-1-085CPC
? CURRENT APPLICATION NUMBER: US/10/0/000,864
? CURRENT FILING DATE: 2001-10-31
? EARLIER APPLICATION NUMBER: 09/423,890
? EARLIER FILING DATE: 2000-06-03
? EARLIER APPLICATION NUMBER: PCT/US99/05556
? EARLIER FILING DATE: 1999-03-15
? EARLIER APPLICATION NUMBER: USSN 60/078,153
? EARLIER FILING DATE: 1998-03-16
? EARLIER APPLICATION NUMBER: USSN 60/099,165
? EARLIER FILING DATE: 1998-09-04
? NUMBER OF SEQ ID NOS: 38
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 4
? LENGTH: 619
? TYPE: PRT
? ORGANISM: Homo sapiens
? IS-10-000-864-4

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Query Match	6.83;	Score 530;	DB 12;	Length 619;
Best Local Similarity	26.98;	Pred. No. 5.5e-21;		
Matches 191; Conservative	90;	Mismatches 252;	Indels 176;	Gaps 32;

QY	877	LDGQO--DSTLQ-----ASVDNNLTETENSSP-----ECVTHLEKTG-KGLGATK	919
Dd	1	MDDOQALNSTMJDLAVLHKASRALPSLOETRAKASSPKQNDVAVYKEHNGEKRIILOVT	60
QY	920	LSASSEDIISERLASISVGFSSSTTTT-----TTTEQPKPMVQTKR-----	961
Dd	61	RPVKLEDLERSK-SKIFAGSQMDLHYNNELVIPTQDDIDKAVELDLRSITHMSLKILL	119
QY	962	-----PHASQCLNNSPLSHSQMLFPAALSPRSSSTPVPACGTATDVSKHNLQ	1007
Dd	120	VWNGSTQATNLEPSPSPEDENNTPLGAERKKALSVAGPPNRRDRSSPPPGYIPD-ELHQIDA	178
QY	1008	---GFIPCR-----IPASAPOTQRFKSTLOFHRNCEKNKDSKLSLSEVFQSPHLESSNIHR	1059
Dd	179	RNGSFTSINSEGEFIPESMDQMLDPLSL---SSPENSGSGSCPSL--DSTLDGSESY-	229
QY	1060	PKRSRTPGCTSKQGPSPKSNKSMPTLDLNSSKCKDDSGGSS-----NSSNA	1104
Dd	230	PKSRMP-----RAQSPYDNHGOETDID--NPTEEFKGAGTVPRRYHVSYHHOEXNGRK	282
QY	1105	VIRSDEVTFPVBEKCRLLVNTNELNSSIIDLLEAMSPSSDTVPFKSEVAVLSPKAEKD	1164
Dd	283	TTFP-----RARRTQGTSTFRSPV-----SFSPTDHLSSGSSSVFTPE----	320
QY	1165	DTYKDDVNHQCKEKEKEAEDEEBALAIAMAMASODALPIVPOLOVENGEDIIIIIOQDP	1224
Dd	321	---YDD-----SMMR-----RRGSDI-----DNP	336
QY	1225	E-TLPGHTAKOPYREDTEMLGGOOIGLGFASGQYQADVGITGLMAKQVTVYRNTSS	1283
Dd	337	TLTVTDSPPCRSPRAPFTMMRLGKLLIGQSDFERVYLICDVTGRLAYAKOVQF-NPESPE	395
Y	1284	QEEVEALREETIRMSHLNHPNITIRMLGATC---EKSYNLFIETMAGGSAVHALLSKYG	1319

Search completed: December 20, 2002, 16:28:58
Job time : 29 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:45 ; Search time 21 Seconds
(without alignments)
2118.450 Million cell updates/sec

Title: US-09-697-898-2
Perfect score: 7825
Sequence: 1 MAAAGNRASSSGPGARAT.....PDRPPRELLKHPVFTTW 1512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6912.5	88.3	1493	4 US-09-423-890-8	Sequence 8, Appl
2	6667	85.2	1593	4 US-08-628-829-4	Sequence 4, Appl
3	6318.5	80.7	1302	4 US-09-423-890-2	Sequence 2, Appl
4	3102.5	39.6	672	1 US-08-049-254-2	Sequence 2, Appl
5	3102.5	39.6	672	1 US-08-472-934-2	Sequence 2, Appl
6	3102.5	39.6	672	2 US-08-323-460A-2	Sequence 2, Appl
7	3102.5	39.6	672	2 US-08-461-145C-2	Sequence 2, Appl
8	3102.5	39.6	672	3 US-08-461-145C-2	Sequence 2, Appl
9	3102.5	39.6	672	4 US-08-628-829-2	Sequence 2, Appl
10	359	7.1	626	1 US-08-472-934-6	Sequence 6, Appl
11	559	7.1	626	2 US-08-323-460A-6	Sequence 6, Appl
12	559	7.1	626	2 US-08-461-145C-6	Sequence 6, Appl
13	559	7.1	626	3 US-08-461-145C-6	Sequence 6, Appl
14	559	7.1	626	4 US-09-423-890-12	Sequence 12, Appl
15	559	7.1	626	4 US-08-628-829-10	Sequence 10, Appl
16	543	6.9	619	1 US-08-472-934-12	Sequence 12, Appl
17	543	6.9	619	2 US-08-461-146C-12	Sequence 12, Appl
18	543	6.9	619	3 US-08-461-145C-12	Sequence 12, Appl
19	543	6.9	619	4 US-08-628-829-8	Sequence 8, Appl
20	534.5	6.8	626	4 US-09-423-890-6	Sequence 6, Appl
21	531	6.8	619	1 US-08-472-934-4	Sequence 4, Appl
22	531	6.8	619	2 US-08-323-460A-4	Sequence 4, Appl
23	531	6.8	619	2 US-08-461-146C-4	Sequence 4, Appl
24	531	6.8	619	3 US-08-461-145C-4	Sequence 4, Appl
25	531	6.8	619	4 US-09-423-890-10	Sequence 10, Appl
26	531	6.8	619	4 US-08-628-829-6	Sequence 6, Appl
27	530	6.8	619	4 US-09-423-890-4	Sequence 4, Appl

28	478	6.1	1247	1 US-08-472-934-10	Sequence 10, Appl
29	478	6.1	1247	2 US-08-323-460A-10	Sequence 10, Appl
30	478	6.1	1247	2 US-08-461-146C-10	Sequence 10, Appl
31	478	6.1	1247	3 US-08-461-145C-10	Sequence 10, Appl
32	475	6.1	1597	4 US-09-423-890-13	Sequence 13, Appl
33	475	6.1	1597	4 US-08-628-829-14	Sequence 14, Appl
34	433	5.5	890	1 US-08-472-934-8	Sequence 8, Appl
35	433	5.5	890	2 US-08-323-460A-8	Sequence 8, Appl
36	433	5.5	890	2 US-08-461-145C-8	Sequence 8, Appl
37	433	5.5	890	3 US-08-461-145C-8	Sequence 8, Appl
38	433	5.5	890	4 US-08-628-829-12	Sequence 12, Appl
39	427.5	5.5	1375	4 US-09-171-410-1	Sequence 1, Appl
40	389.5	5.0	403	2 US-08-755-728-4	Sequence 1, Appl
41	389.5	5.0	403	3 US-08-974-655-4	Sequence 4, Appl
42	389.5	5.0	403	4 US-09-283-011-4	Sequence 4, Appl
43	378.5	4.8	524	2 US-08-615-942A-2	Sequence 2, Appl
44	376.5	4.8	545	2 US-08-935-760-4	Sequence 4, Appl
45	374.5	4.8	544	2 US-08-935-760-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-423-890-8
Sequence 8, Application US/09423890
Patent No. 6312934
GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OR INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
FILE REFERENCE: CPI-085CPC
CURRENT APPLICATION NUMBER: US/09/423,890
CURRENT FILING DATE: 2000-03-06
PRIORITY APPLICATION NUMBER: USSN 60/078,133
PRIORITY FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: USSN 60/099,165
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1493
TYPE: PRT
ORGANISM: Mus musculus
US-09-423-890-8

Query Match	88.3%	Score 6912.5	DB 4	Length 1493
Best Local Similarity	89.5%	Pred. No. 0		
Matches 1358	Conservative 47	Mismatches 82	Indels 31	Gaps 11
QY 1	MAAAGNRASSSGPGARATSPFA---GGGGALAKASAPAA-AAAGLREAGSGGERAD	56		
DB 1	MAAAGNRASSSGPGARATSPFA---GGGGALAKASAPAA-AAAGLREAGSGGERAD	60		
QY 57	WRRRLKRVRSVELDQLEPQPLFL-ASPPASSTSPSPEDPAAGSGTGQPAVAPPHG	115		
DB 57	WRRRLKRVRSVELDQLEPQPLFL-ASPPASSTSPSPEDPAAGSGTGQPAVAPPHG	120		
QY 61	WRRHVRVRSVELDQLEPQPLFLAASPPCSTSPSPEDPAAGSARFQPAAGPPPG	120		
DB 61	WRRHVRVRSVELDQLEPQPLFLAASPPCSTSPSPEDPAAGSARFQPAAGPPPG	175		
QY 116	AASRGALHTSVAAPOSGASPPAAEPGEKRAAEPSPAAAGRMEKKTLLGLHK	175		
DB 116	AASRGALHTSVAAPOSGASPPAAEPGEKRAAEPSPAAAGRMEKKTLLGLHK	170		
QY 121	AASRGASISALAAARSGARSPPAGAP-----PS-AAAPSGRMEKKTLLGLHK	235		
DB 121	AASRGASISALAAARSGARSPPAGAP-----PS-AAAPSGRMEKKTLLGLHK	230		
QY 176	MDDPPEEMIEKTKATCMPAKHEMLERRNRGPVYVKPIPVKGDGSEMHAAESPGE	295		
DB 176	MDDPPEEMIEKTKATCMPAKHEMLERRNRGPVYVKPIPVKGDGSEMHAAESPGE	290		
QY 231	QOASGSAAPAPKGRSPSPGSSPSGRSVKPESPGYRRKRVSPVPOSGRTTPPRAPSPDG	290		
DB 231	QOASGSAAPAPKGRSPSPGSSPSGRSVKPESPGYRRKRVSPVPOSGRTTPPRAPSPDG	355		
QY 296	FSPTSPETSRKRVKVMARLYLLQOIGPNSFLIGDSDPKKRVVFVFGPONGCARGTFC	350		
DB 296	FSPTSPETSRKRVKVMARLYLLQOIGPNSFLIGDSDPKKRVVFVFGPONGCARGTFC			

QY 356 IHLPLVMLRVFQLEPBDPLMKRTLKNEFVESLFQYHSRSGSRKAPSRNTIQKTVSM 415
DB 351 IHLPLVMLRVFQLEPBDPLMKRTLKNEFVESLFQYHSRSGSRKAPSRNTIQKTVSM 410
QY 416 SNHSHTSSSTSSSESENKDEEOMCPICLLGMDESLVYCEGCKNKLHHHMCSTM 475
DB 411 SNHSHTSSSTSSSESENKDEEOMCPICLLGMDESLVYCEGCKNKLHHHMCSTM 470
QY 476 AEECRNRREPLICPLCRSMRSHDFYSHELSPVDSPLRAAOQOTVOOPLAGS-RRN 534
DB 471 AEECRNRREPLICPLCRSMRSHDFYSHELSPVDSPLRAVOQDSSPOQVAGSQORN 530
QY 535 QSSNRRLTHYGTOQIPRAKDLAEPIYQFGMELVGCLESRRMNNREMLRLSHDVSA 594
DB 531 QSSNRRLTHYGTOQIPRAKDLAEPIYQFGMELVGCLESRRMNNREMLRLSHDVSA 590
QY 595 LLLANGESTGNSGGSGSSPSGATSGSSQTSISGDVYACCSVLSMWCADVYKYVVA 654
DB 591 LLLANGESTGNSGGSGSSPSGATSGSSQTSISGDVYACCSVLSMWCADVYKYVVA 650
QY 655 LKTRAMLVYTPCHSLAERIKLQRLQPVDTLVKCADANSRTSOLISTLELCKGOA 714
DB 651 LKTRAMLVYTPCHSLAERIKLQRLQPVDTLVKCADANSRTSOLISTLELCKGOA 710
QY 715 GELANGRELKAGSIGIGVYVYVNCILGNQTESNMWOLGRLCLIDRLLEFPAEFP 774
DB 711 GELANGRELKAGSIGIGVYVYVNCILGNQTESNMWOLGRLCLIDRLLEFPAEFP 770
QY 775 HVTSTDVSOAEVEIRKYLKLSLTFALQSIINSHSMVGLSRRTYLSARWYTPVHF 834
DB 771 HVTSTDVSOAEVEIRKYLKLSLTFALQSIINSHSMVGLSRRTYLSARWYTPVHF 830
QY 835 SKLLEMLSVSSSTHFTMRRLMAIADVEVIAEIQLVGEDTLGQODSFLQASVNNYL 894
DB 831 SKLLEMLSVSSSTHFTMRRLMAIADVEVIAEIQLVGEDTLGQODSFLQASVNNYL 889
QY 895 ETTENSPECTVHLEKGTGCLATKLSASEDISERLASISVGPSSSTTTTTTQORP 954
DB 890 ETTENSPECTVHLEKGTGCLATKLSASEDISERLASISVGPSSSTTTTTTQORP 941
QY 955 MYOTGRPSHOCILNSSPLSHSOLMPALSTPSSSTPSPACTATVYSHKRLQGFPCR 1014
DB 942 MYOTGRPSHOCILNSSPLSHSOLMPALSTPSSSTPSPACTATVYSHKRLQGFPCR 995
QY 1015 PSASPOTQKFFSLQFHRCNCPENKSDKLSPVFTQSRPLSSNHRKPSRPPTGNTSKG 1074
DB 996 PSASPOTQKFFSLQFHRCNCPENKSDKLSPVFTQSRPLSSNHRKPSRPPTGNTSKG 1055
QY 1075 DSKNSMTIDLSSSKCDSFGCSSSNNAVTPSDETVFTPYECKRLDVNTELSSTD 1134
DB 1056 DSKNSMTIDLSSSKCDSFGCSSSNNAVTPSDETVFTPYECKRLDVNTELSSTD 1115
QY 1135 LLEASPSDDTYVTFKSEVAVALSPEKAENDDYKDDVNNOKCKEMEAESEBALAIANA 1194
DB 1116 LLEASPSDDTYVTFKSEVAVALSPEKAENDDYKDDVNNOKCKEMEAESEBALAIANA 1175
QY 1195 MSASODALPIVPOLOVENEDIIIIQODTPETLPGHTTKAKOPYREDETEMLKQOQIGLAF 1254
DB 1176 MSASODALPIVPOLOVENEDIIIIQODTPETLPGHTTKAKOPYREDETEMLKQOQIGLAF 1235
QY 1255 SSCYQAOVGTGTMAVKVYTVVRNTSSSQEVEVEALREIEMSLNPNIIIMLGATC 1314
DB 1236 SSCYQAOVGTGTMAVKVYTVVRNTSSSQEVEVEALREIEMSLNPNIIIMLGATC 1295
QY 1315 EKSNTNLEFEMMAGSVAILLSKYGAFKESVYINTTEOLLRGTSYHEHQIIRHDVKGAN 1374
DB 1296 EKSNTNLEFEMMAGSVAILLSKYGAFKESVYINTTEOLLRGTSYHEHQIIRHDVKGAN 1355
QY 1375 LLIDSTGQRLRIADFGAAARLASKGTAGEFQGLGTIAFNAPEVLRGOQVGRSCDVS 1434
DB 1356 LLIDSTGQRLRIADFGAAARLASKGTAGEFQGLGTIAFNAPEVLRGOQVGRSCDVS 1415

QY 1435 VGCATIEMACAPPMNAEKSHNLALIFKIASATTAPSPHLSRGLDVALRCLELOPO 1494
DB 1416 VGCATIEMACAPPMNAEKSHNLALIFKIASATTAPSPHLSRGLDVALRCLELOPO 1475
QY 1495 DRPPRELLKHVPFRFTW 1512
DB 1476 DRPPRELLKHVPFRFTW 1493

RESULT 2
US-08-628-829-4
Sequence 4, Application US/08628829A
Patent No. 6333170
GENERAL INFORMATION:
APPLICANT: Johnson, Gary L.
TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To Exter
FILE REFERENCE: CPI-004DVC3
CURRENT APPLICATION NUMBER: US/08/628,829A
EARLIER FILING DATE: 1996-04-05
EARLIER APPLICATION NUMBER: 08/440,421
EARLIER FILING DATE: 1995-05-15
EARLIER APPLICATION NUMBER: 08/323,460
EARLIER FILING DATE: 1994-10-14
EARLIER APPLICATION NUMBER: 08/049,254
EARLIER FILING DATE: 1993-05-15
EARLIER APPLICATION NUMBER: 08/410,602
EARLIER FILING DATE: 1995-04-24
EARLIER APPLICATION NUMBER: 08/472,934
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 1593
TYPE: PRT
ORGANISM: Mus musculus
US-08-628-829-4

Query Match 85.2%; Score 6667; DB 4; Length 1593;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1322; Conservative 49; Mismatches 102; Indels 58; Gaps 13;

QY 1 MAAAGNRASGSGFGARATSPESA---GGGGALAKASSAPAA-ANGILREAGSGRERAD 56
DB 102 MAAAGNRASGSGFGARATSPESA---GGGGALAKASSAPAA-ANGILREAGSGRERAD 161
QY 57 -----WRRQLRKRSVLELDQLEPDLFLAASPASTSPSPADAGSGTGF 105
DB 162 GGGGTCACKGVSWTSCRSRS-----SSPPRRPAHLPLVAGARRGCRS 207
QY 106 QPV---AVPPRGAASRGGAHLTESVAAPDGCASSPAAAEPECKRAPAAEPSPAAPAGR 162
DB 208 ESLPARAGPPPGAASRCGSHAEIILAAARDGARSPPAGAE-----PS-AAAPSGR 257
QY 163 EMEKETTGLKMKDDRPEREMIRREKIKATCMPAMKHEMLERRNRGVPVYVPIYKGDG 222
DB 258 EMEKETTGLKMKDDRPEREMIRREKIKATCMPAMKHEMLERRNRGVPVYVPIYKGDG 317
QY 223 SEMNLAAESPGEVQASAASPAASKGRSPSPGNSPGRTVKSSESPGVRRKRVSPVPQSG 282
DB 318 SEMNLAAESPGEVQASAASPAASKGRSPSPGNSPGRTVKSSESPGVRRKRVSPVPQSG 377
QY 283 RTTPRRRASPDPGFSFYSPSEETNRNRVKNYMARLYLLOOIGNSFLIGDSDPNKRYRVI 342
DB 378 RTTPRRRASPDPGFSFYSPSEETNRNRVKNYMARLYLLOOIGNSFLIGDSDPNKRYRVI 437
QY 343 GPONSCAGTCFCHLLFVMLRVFQLEPBDPLMKRTLKNEFVESLFQYHSRSGSRKA 402
DB 438 GPONSCAGTCFCHLLFVMLRVFQLEPBDPLMKRTLKNEFVESLFQYHSRSGSRKA 497
QY 403 PSRNTIQKTVSMNSHTLSSSSTSSSESENKDEEOMCPICLLGMDESLVYCEG 462
DB 498 PSRNTIQKTVSMNSHTLSSSSTSSSESENKDEEOMCPICLLGMDESLVYCEG 557

QY	463	C R N K L H H C H S I A I B E C R R R R E P L I C P L C R S W R S H D T Y S H E L S P S P D S S L F A A O O T	522
QY	463	C R N K L H H C H S I A I B E C R R R R E P L I C P L C R S W R S H D T Y S H E L S P S P D S S L F A A O O T	522
Db	558	C R N K L H H C H S I A I B E C R R R R E P L I C P L C R S W R S H D T Y S H E L S P S P D S S L F A A O O P S	617
QY	523	V O O P L A G S - R R N O E S N F N L T H T G O I P P A K D L A E P I O V F G E L V G C F S R N M V N R E	581
Db	618	S P O O P V A G S O R R N O E S F N L T H T G O I P S A K D L A E P R I O V F G E L V G C L F S R N M V N R E	677
QY	582	M A L R L S H D V S G A L L L A N G E S T G N S G S G S S P S G A T S S G S S O T S I S G D V E A C C S Y L S M	641
Db	678	M A L R L S H D V S G A L L L A N G E S T G N S G S G S G S L S G A A S G S S O P S I S G D V E A C C S Y L S I	737
QY	642	V C A P P V K Y V V A A L K T L R A L V Y T P C H S I A E R I K I O R L L O P V P V D I L Y K C A D A N S R I S O L	701
Db	738	V C A P P V K Y V V A A L K T L R A L V Y T P C H S I A E R I K I O R L L R P V D I L Y K C A D A N S R I S O L	797
QY	702	S I S T L E L C K G O A G E L A V R E I L K A G S I S I G D V Y V L N C I G N O T E S N M M O E L L G R C L I	761
Db	798	S I S T V L E L C K G O A G E L A V R E I L K A G S I G V G D V Y L S C I I G N A E S N M M O E L L G R C L I	857
QY	762	D R L L E P P A E F Y P H I Y S T D V S O A E P E I T K U L S I L T P A L O S I D N S S M Y G K I S R I Y L	821
Db	858	D R L L E P P A E F Y P H I Y S T D V S O A E P E I T K U L S I L T P A L O S I D N S S M Y G K I S R I Y L	917
QY	822	S S A M V T V V H V S F S K L E M L S V S S T H F T R M R R L M A I D E V E I A E A I O L E V D T P L G O O	881
Db	918	S S A M V T A V A V S K L Y T M L N A S G S H F T R M R R L M A I D E V E I A E V I O L E V D T P D H Q	977
QY	882	D S F L O A S P N N Y L E T T E N S S P E C T V H L E K T G K L C A T K L S A S S E D I S E R L A S I S V P S S	941
Db	978	D S - L O A V A P I S C L - - E N S L E H T V H R E K T G K L S A T R L S A S S E D I S R L A G S V S L P S S	1033
QY	942	T T T T T T T E D P K M Y O T K G P H S O C N S S P L S H S O L M P A L S T P S S S T P E V P A G I A T A D V	1001
Db	1034	- - - - - T T E O K P R P V O T K G P H S O C N S S P L S - H A O L M P A S A C S S A P S P - - - - - D I	1082
QY	1002	S K H R L O G F I P C R I P S A S P O T O R K F S L O F P R N C P E N K D S D K L S P V T O S R P L P S S N I H R P K	1061
Db	1083	S K H P O A F V P O C K I P S A S P O T O R K F S L O F O R N C S E H R D S O L S P V T O S R P P S S N I H R P K	1142
QY	1082	P S R T P E N T S K O Q D P S K N S M T L D L N S S K C D D S F G C S S N S S A N V I P S D E Y F T P Y E K E C R	1121
Db	1143	P S R P V P S T S L S D A T K S M T L D L S G A S C D D S F G G G G S N A V I P S D E Y F T P Y E D C R	1202
QY	1122	L D V T E L N S S I E D L E A S M P S D T Y T F F S E V A V L S P E K A E N D D Y P K D V N H N O K C K E M	1181
Db	1203	L D V T E L N S S I E D L E A S M P S D T Y T F F S E V A V L S P E K A E N D D Y P K D V N H N O K C K E M	1262
QY	1182	E A E E B E A L A I A M A M S A S O D A L P I V P O L O V N G E D I I I I O Q D T P E T L P G H T A K O P Y R E D T	1241
Db	1263	E A E E E B E A L A I A M A M S A S O D A L P I V P O L O V N G E D I I I I O Q D T P E T L P G H T A K O P Y R E D A	1322
QY	1242	E M L G O O I G I G A S S C C O A D V G T G L M A V K O T T Y V R N T S S O E E V N A L E E E I R M S H L	1301
Db	1323	E M L G O O I G I G A S S C C O A D V G T G L M A K O V T T Y V R N T S S O E E V N A L E E I R M M G H L	1382
QY	1302	N H P N I I R M L G A T C E K S N Y N L F I E M A M G G S V A H L S K Y G A F K E S V Y I N T E O L R G L S T Y L H	1361
Db	1383	N H P N I I R M L G A T C E K S N Y N L F I E M A M G G S V A H L S K Y G A F K E S V Y I N T E O L R G L S T Y L H	1442
QY	1362	E N O I I I H D V K A N L L D S T S O Q R L R I A D F G A A A R A L A S K G T G A G E P O G O L L G T I A P M A P V L	1421
Db	1443	E N O I I I H D V K A N L L D S T S O Q R L R I A D F G A A A R A L A S K G T G A G E P O G O L L G T I A P M A P V L	1502
QY	1422	R G O O Y G R S C D W S V G C A I I E M A C A K P P M A E K S N H L A I F R I A S A T T A P S I P S H L S G L	1481
Db	1503	R G O O Y G R S C D W S V G C A I I E M A C A K P P M A E K S N H L A I F R I A S A T T A P S I P S H L S G L	1562
QY	1482	R D V A L R C L E I O P O D R P S R E L L K H P V F R T T W	1512
Db	1563	R D V A V R C L E I O P O D R P S R E L L K H P V F R T T W	1593

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RESULT 3
US-09-423-890-2
; Sequence 2, Application US/09423890
; Patent No. 6312934
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: CPI-085CEPC
; CURRENT APPLICATION NUMBER: US/09/423, 890
; CURRENT FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: USSN 60/078,153
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: USSN 60/099,165
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO. 2
; LENGTH: 1302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-890-2

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OY 856 LMAADEVEIAEAIQIGVEDTLGGQQDSFLQASVPNNYLETTENSSPECTVHLKTKTGL 915
||||| : ||||| : |||||

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Db 661 LMAIADEVEIAEVIQGVEDIVDGHODS-LQALAPASCL---ENSSLEHTVHREKTKGCL 716
QY 916 CATKLSASSEDISERLASISVGPSSSTTTTTEQPKPMVQTKGRPHSQCINSSPLSHH 975
Db 717 SATRLSASSEDISDRLAGVSGVLPSS-----TTTEQPKPMVQTKGRPHSQCINSSPLS-H 770
QY 976 SOLMPALSTPSSPSPVAGTATDVSKHRLQCFICRIPASAPQORFSLQFHNCPRE 1035
Db 771 AQLMFPAPSPASSAPSV-----DISKHPQAFVPCKIPASAPQORFSLQFHNCPRE 825
QY 1036 NKDSKLSVFTQSRPLPSSNIHRKPSRPTPGNTSKQDPSKNSMTLDLNSSKCDSPF 1095
Db 826 HSDSDQLSVFQSRPSPSSNIHRKPSRPTPGNTSKQDPSKNSMTLDLNSSKCDSPF 885
QY 1096 GCSNSSNNAVDSDEVTFTVPEEKCRLDVNTLNSIEDLLEASMPSSDTTTFKSEVAV 1155
Db 886 GCGGSGNNAVIPSDEVTFTVPEEKCRLDVNTLNSIEDLLEASMPSSDTTTFKSEVAV 945
QY 1156 LSPKENDDTYKDDVNNHOKCKEKEAEDEEALATAMMASQDALPTVPOLQVENGED 1215
Db 946 LSPKENDDTYKDDVNNHOKCKEKEAEDEEALATAMMASQDALPTVPOLQVENGED 1005
QY 1216 IIIIQDPTETLPKHTKAKQPYREDEWEMLKGOQIGLAFSSCYQADVGITIMAVKQYT 1275
Db 1006 IIIIQDPTETLPKHTKAKQPYREDEWEMLKGOQIGLAFSSCYQADVGITIMAVKQYT 1065
QY 1276 YVRNTSSEDEVEEVALREIRRMWSHLNHPNIIIRMGATCEKSNYNLFITEMAGSVAHLL 1335
Db 1066 YVRNTSSEDEVEEVALREIRRMWSHLNHPNIIIRMGATCEKSNYNLFITEMAGSVAHLL 1125
QY 1336 SKYGAKESVINYTPQRLRGISYLHENQIIRHDVGANLLIDSTQORLIRADFGAAARL 1395
Db 1126 SKYGAKESVINYTPQRLRGISYLHENQIIRHDVGANLLIDSTQORLIRADFGAAARL 1185
QY 1396 ASKGTCAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCALIIEMACAKPPWNAEKHS 1455
Db 1186 ASKGTCAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCALIIEMACAKPPWNAEKHS 1245
QY 1456 NHALIFKIASATTAPISHSPLGRDVALRCLLEQPODRPSSRELKHPVFRRTW 1512
Db 1246 NHALIFKIASATTAPISHSPLGRDVALRCLLEQPODRPSSRELKHPVFRRTW 1302

RESULT 4
US-08-049-254-2
; Sequence 2, Application US/08049254
; Patent No. 5405941
; GENERAL INFORMATION:
; APPLICANT: Johnson Ph.D., Gary L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH, P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,254
; FILING DATE: 19930415
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik Esq., Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-1
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; TELEX: 467377
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 672 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-049-254-2

Query Match      39.6%; Score 3102.5; DB 1; Length 672;
Best Local Similarity 89.2%; Pred. No. 66-194;
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY 826 MTTTTPHVSFKLEMLSVSSSTHTFRMRRLMAIAEVEIAEVIQGVEDIVDGHODSFL 885
Db 1 MTTTTPHVSFKLEMLSVSSSTHTFRMRRLMAIAEVEIAEVIQGVEDIVDGHODS-L 59
QY 886 QASVNNVLETENNSSPECTVHLEKTKGICATKLSASSEDISERLASISVGPSSSTTTT 945
Db 60 QAVAPTSCL---ENSSLEHTVHREKTKGISATRLSASSEDISDRLAGVSGVLPSS----- 112
QY 946 TTTTEQPKPMVQTKGRPHSQCINSSPLSHSOLMPALSTPSSSTPSVAGTATDVSKHR 1005
Db 113 -TTTEQPKPMVQTKGRPHSQCINSSPLS-HAQLMFPAPSPASSAPSV-----DISKHR 165
QY 1006 LQGFICRIPASAPQORFSLQFHNCPENKSDKLSVFTQSRPLPSSNIHRKPSRP 1065
Db 166 PQAIFVCKIIPASAPQORFSLQFHNCPENKSDKLSVFTQSRPLPSSNIHRKPSRP 225
QY 1066 TPGNTSKQDPSKNSMTLDLNSKCDSPFSGCSNSSNNAVIPSDEVTFTVPEEKCRLDVN 1125
Db 226 VPGSTSKLDGATKSSMTLLDGASRCDSPFSGGSGNNAVIPSDEVTFTVPEEKCRLDVN 285
QY 1126 TELNSSIEDLEASMPSSDTTTFKSEVAVLSPKENDDTYKDDVNNHOKCKEKEAE 1185
Db 286 TELNSSIEDLEASMPSSDTTTFKSEVAVLSPKENDDTYKDDVNNHOKCKEKEAE 345
QY 1186 EELATAMMASQDALPTVPOLQVENGEDIIIIQDPTETLPKHTKAKQPYREDEWEMLK 1245
Db 346 EELATAMMASQDALPTVPOLQVENGEDIIIIQDPTETLPKHTKAKQPYREDEWEMLK 405
QY 1246 GQOIGLAFSSCYQADVGITIMAVKQYTYRNTSSEDEVEEVALREIRRMWSHLNHPN 1305
Db 406 GQOIGLAFSSCYQADVGITIMAVKQYTYRNTSSEDEVEEVALREIRRMWSHLNHPN 465
QY 1306 IIRMGATCEKSNYNLFITEMAGSVAHLLSKYGAKESVINYTPQRLRGISYLHENQI 1365
Db 466 IIRMGATCEKSNYNLFITEMAGSVAHLLSKYGAKESVINYTPQRLRGISYLHENQI 525
QY 1366 IIRHDVGANLLIDSTQORLIRADFGAAARLASKGTCAGEFQGLGTIAFMAPEVLRGQO 1425
Db 526 IIRHDVGANLLIDSTQORLIRADFGAAARLASKGTCAGEFQGLGTIAFMAPEVLRGQO 585
QY 1426 YGRSCDWSVGCALIIEMACAKPPWNAEKHSNHALIFKIASATTAPISHSPLGRDVA 1485
Db 586 YGRSCDWSVGCALIIEMACAKPPWNAEKHSNHALIFKIASATTAPISHSPLGRDVA 645
QY 1486 LRCLEQPODRPSSRELKHPVFRRTW 1512
Db 646 VRCLEQPODRPSSRELKHPVFRRTW 672

RESULT 5
US-08-472-934-2
; Sequence 2, Application US/08472934
; Patent No. 5753446
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
; NUMBER OF SEQUENCES: 12

```

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,934
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/440,421
FILING DATE: 15-May-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/354,516
FILING DATE: 21-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 5,405,941
FILING DATE: 15-Apr-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/323,460
FILING DATE: 14-Oct-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-Oct-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. Decontii, Jr. Esq.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: CPT-004DVCPE2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 672 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-934-2

Query Match          39.6%; Score 3102.5; DB 1; Length 672;
Best Local Similarity 89.2%; Pred. No. 6e-194;
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY 826 MATTVAHVSVSKLLEMLSVSSSTHFTRRRLMAIADEVETAEALIQGVEDTLTGQDSFL 885
DB 1 MTTVAHVSVSKLLEMLSVSSSTHFTRRRLMAIADEVETAEALIQGVEDTLTGQDSFL 59
QY 886 QASVPMNYLETTESSSPECTVHLEKTKGKCATRKLSASSSDISPRLASISVGPSSSTTTT 945
DB 60 QAVAPTSCL--ENSLIEHTVHREKTKGKLSATRLSSASSDISPRLAGVSGLDPS---- 112
QY 946 TTTTEOPKPAVOTKGRPHSOCLNSSLSPSHSOLMFALSTPSSSTPSVPAQTADVSKHR 1005
DB 113 -TTTEOPKPAVOTKGRPHSOCLNSSLSPSHSOLMFALSTPSSSTPSVPAQTADVSKHR 165
QY 1006 LOGFICRITISASPTQOKRSLQFHRKCPENKSKSDKSLPFTQSRPLPSSNIHRPKSRP 1065
DB 166 PQAFVPCPKIPSPQOTOKRSLQFHRKCPENKSKSDKSLPFTQSRPLPSSNIHRPKSRP 225
QY 1066 TPENTSKQGPKNKSMWTLIDNSSSKCDSPGSCSSNSSNAVIPSDEYFTVEEKCRLDVN 1125
DB 226 VPSTSKLGDATKSSMTLIDGASASRCDDSRGGGSGNSGNNAVIPSDEYFTVEEKCRLDVN 285

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QY 1126 TELNSSIEDLLEASMPSSDTTTFKSEVAVALSPEKAEENDTYDDVNHNOCKEKEAE 1185
DB 286 TELNSSIEDLLEASMPSSDTTTFKSEVAVALSPEKAEENDTYDDVNHNOCKEKEAE 345
QY 1186 EELATAMAMASODALPIYPOLOVENGEDIIITQDPTPLGHTAKOPYREDTBLK 1245
DB 346 EELATAMAMASODALPIYPOLOVENGEDIIITQDPTPLGHTAKOPYREDTBLK 405
QY 1246 GQOIGLGFSSCYOAOQDVGTGLMAVKQTYVRNTSSQSEVEEALREIRMSHLNHPN 1305
DB 406 GQOIGLGFSSCYOAOQDVGTGLMAVKQTYVRNTSSQSEVEEALREIRMSHLNHPN 465
QY 1306 IIRMLGATCEKSNVNIETEMAGGSVAHLISKYGAFFESVYINTEQLGLSTLHENQI 1365
DB 466 IIRMLGATCEKSNVNIETEMAGGSVAHLISKYGAFFESVYINTEQLGLSTLHENQI 525
QY 1366 IHRDVKANLLIDSTGRLTIADFGAARLASKGTGAGEFOGLGTLIARMAEVLRGQO 1425
DB 526 IHRDVKANLLIDSTGRLTIADFGAARLASKGTGAGEFOGLGTLIARMAEVLRGQO 585
QY 1426 YGRSCDVWSYGCAIIEMACAKPPMAEKHSNHLALIKRIASATTAPISPSHLSGLRDVA 1485
DB 586 YGRSCDVWSYGCAIIEMACAKPPMAEKHSNHLALIKRIASATTAPISPSHLSGLRDVA 645
QY 1486 LRCLLELOPQDRPPSRELLKHVFRTTW 1512
DB 646 VRCLLELOPQDRPPSRELLKHVFRTTW 672

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RESULT 6
US-08-323-460A-2
Sequence 2, Application US/08323460A
Patent No. 5854043
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
RESPONSIVENESS TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS & MCINTOSH
STREET: 1700 LINCOLN STREET, SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,460A
FILING DATE: 14-Oct-1994
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 14-Apr-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 672 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-460A-2

Query Match          39.6%; Score 3102.5; DB 2; Length 672;

```

Best Local Similarity 89.2%; Pred. NO. 6e-194;
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

OY	826	MYTTPHYEKSLEMLSVSSSTHFFRMRRRLMAIDVEYIAIAIOLGVDDTLGOODSTL	885
Db	1	MYTAYPAFYSKLVYMLNMGSTHFFRMRRRLMAIDVEYIAEYIOLGVDDIYDGHODS-L	59
OY	886	QASVNNVLETTENSSPECTVAHLEKYGOLCATKLASSSEDISERLASISVGPSSSTYTT	945
Db	60	QAVATPSTCL---ENSSLEHTVHREKTGKGLASTRLSASEDISDRLAGVGLPSS----	112
OY	946	TTTTPOPKPMVOTKCRPHSOCNSSPLSHSOMLPALTSPSSSPSYAGCATIYVSKHR	1005
Db	113	TTTTQPKPFAVOTKCRPHSOCNSSLPLS-HAOLMPAPASCPSSAPSV---DISKRR	165
OY	1006	LOGFIPCRIPASPOTORKFSLOQFRRNCPENDSDSKLSBVFQSKRPLPSNTHRPKPSR	1065
Db	166	POAFVPCRKIPASPOQRKFSLOQFRRNCEHHRDSDQLSVFQSKRPPSSNTHRPKPSR	225
OY	1066	TPGNSTSKGDDPSKNSMTLDLNNSSKCDSPGCCSSNNSNAVIPSDETVTPPVECKRLDVN	1125
Db	226	VPGSTSKLGDAKSSMTLDDLGSASCDSPGCGGSGNSNAVIPSDETVTPVVDKCRLDVN	285
OY	1126	TELNSSIEDLEASMPSSDVTYTFKSEVAVLSPEKAENDTYKDDVNNHOKCKEKEABE	1185
Db	286	TELNSSIEDLEASMPSSDVTYTFKSEVAVLSPEKAENDTYKDDVNNHOKCKEKEABE	345
OY	1186	EEALIAAMASASODALPIVPOLOVENGEDIITIOODTPETLPGHTAKOPYREDTEWLK	1245
Db	346	EEALIAAMASASODALPIVPOLOVENGEDIITIOODTPETLPGHTAKOPYREDTEWLK	405
OY	1246	GOOIGLGAFFSSCYAODDGTGFLMAVKOVTYVRNNTSROEEVVEALAREIRMSHNLNPN	1305
Db	406	GOOIGLGAFFSSCYAODDGTGFLMAVKOVTYVRNNTSROEEVVEALAREIRMSHNLNPN	465
OY	1306	IIRMLGATCEKSNVNLFTEMMAGGSVAHLLSKYGAFKESVNVINTEQLRLGLSYLHENOI	1365
Db	466	IIRMLGATCEKSNVNLFTEMMAGGSVAHLLSKYGAFKESVNVINTEQLRLGLSYLHENOI	525
OY	1366	IHRDVKGNLILDSGOURLRINDPEGAARLASKGAGAEFGQOLLGTTAFMPEVLRGOQ	1425
Db	526	IHRDVKGNLILDSGOURLRINDPEGAARLASKGAGAEFGQOLLGTTAFMPEVLRGOQ	585
OY	1426	YGRSCDVMSVGCALIEEMACAKPPMAAEKSHNLALITFKIASATYTPASIPSHSLPGLRDVA	1485
Db	586	YGRSCDVMSVGCALIEEMACAKPPMAAEKSHNLALITFKIASATYTPASIPSHSLPGLRDVA	645
OY	1486	LARCELOQODRPPSRRELLKHPYFRITTW 1512	
Db	646	VNCTELOQODRPPSRRELLKHPYFRITTW 672	

RESULT 7
 US-08-461-146C-2
 Sequence 2, Application US/08461146C
 Patent No. 5981265
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, GARY L.
 TITLE OF INVENTION: METHODS FOR REGULATING MEK1 PROTEIN ACTIVITY
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahniv and Cockfield
 STREET: 60 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER: US/08/461,146C
2  FILING DATE: 05-JUN-1995
3  CLASSIFICATION: 435
4
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: US 08/354,516
7  FILING DATE: 21-FEB-1995
8
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 08/049,254
11 FILING DATE: 15-APR-1993
12
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 08/323,460
15 FILING DATE: 14-OCT-1994
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: PCT/US94/11690
19 FILING DATE: 14-OCT-1994
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: PCT/US94/04178
23 FILING DATE: 15-APR-1994
24
25 ATTORNEY/AGENT INFORMATION:
26 NAME: KARA, Catherine J.
27
28 REGISTRATION NUMBER: P41,106
29 REFERENCE/DOCKET NUMBER: CPT-004C93
30
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (617) 227-7400
33 TELEFAX: (617) 227-5941
34
35 INFORMATION FOR SEQ ID NO: 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 672 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40
41 MOLECULE TYPE: protein
42
43 US-08-461-146C-2

```

Query Match	39.6%	Score 1102.5	DB 2	Length 672
Best Local Similarity	89.2%	Pred. No. 6e194		
Matches 613	Conservative 21	Mismatches 38	Indels 15	Gaps 5
QY 826	MVTVPVHVESKLEMLSVSSSTHFFRRMRRLMALADEVEIAEAQIQAGEEDLDQODSFL	885		
DB 1	MTVAIPAVFESKLVYTMILNMSGSTHFFRRMRRLMALADEVEIAEQIAGEEDVDDHOTS-L	59		
QY 886	QASVNNNTLETTENSSPDCYVHLEKTKGGLCATKILASSEDISERLASISVGPSSSTTTT	945		
DB 60	QAVAPTSQL--ENSSLHPTVHRETKGGLCATRLSASSEDISDRLAGVSGLPSS----	112		
QY 946	TTTTQPKPMYOTKGRPHSQCINSSPLHSHOLMPRALSTPSSSPSPACTADVDSKHR	1005		
DB 113	TTTQPPAPVAYOTKGRPHSQCNSSPL-HAOLMPAPASACSSKSPV-----DISKHR	165		
QY 1006	LOGFIPCRIPSPASPOTORKKFSLQFHRNCPENKDDSKLSPVETQSKPLPSSNIHRPKPSRP	1065		
DB 166	PQAFVPCIKIPSPASPOTORKKFSLQFHRNCSHRDSDQLSPVETQSKPRPSSNIHRPKPSRP	225		
QY 1066	TPGNTSKQGDPSKSNMTLDLNSSKCDSDSFCGSSNSSNAVIPSDETVPTPVEEKCRLDVN	1125		
DB 226	VPGSTSKGDAITKSSMTLDLSCASKCDSDSFCGGGSGNAVIPSDETVPTPEDKCRLDVN	285		
QY 1126	TEINSTEIDLEASMPSSDVTTFESEAVALSPEAEKNDPTKDDVYNNQCKRKEMAEE	1185		
DB 286	TEINSTEIDLEASMPSSDVTTFESEAVALSPEAEKNDPTKDDVYNNQCKRKEMAEE	345		
QY 1186	EEALAIAMASASODALPIVPOLOVENEDIIIIQQDPEPLPGHTAKOPYREDTEMLK	1245		
DB 346	EEALAIAMASASODALPIVPOLOVENEDIIIIQQDPEPLPGHTAKOPYREDTAEMLK	405		
QY 1246	GOQIGLGAFFSSCYAQODVGTGLMAVQVTVYRNTSSEQEEVVALREIRIMSHLHNPN	1305		
DB 406	GOQIGLGAFFSSCYAQODVGTGLMAVQVTVYRNTSSEQEEVVALREIRIMSHLHNPN	465		
QY 1306	IIRHMGATCEKSNYNLFLEMMAGGSVAHLLSKYAFKFSYVINTTEQLRLSLJHENQI	1365		
DB 466	IIRHMGATCEKSNYNLFLEMMAGGSVAHLLSKYAFKFSYVINTTEQLRLSLJHENQI	525		

US-08-628-829-2

Query Match 39.6%; Score 3102.5; DB 4; Length 672;
Best Local Similarity 89.2%; Pred. No. 66-194;
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY 826 MYTVPHVSKLLEMSVSSSTFTFMRRLMAIADEVEIAEAIQGVEDTLDGQDSFL 885
DB 1 MYTAVAVPVSFKLVTMLNAGSTFTFMRRLMAIADEVEIAEAIQGVEDTVGHGDS-L 59
QY 886 QASVPNNYLETTESSPECTVHEKTGKGLCATKLSASSDISERLASISVGPSSSTTT 945
DB 60 QAVAPTSCL---ENSSLEHTVHREKTGKGLSATRLSASSDISDRLAGVSGLPSS---- 112
QY 946 TTTTEQPKPMVOTKGRPHSQCLNSSPLSHHSQMLPALSTPSSSTPSVPAGTADVSKHR 1005
DB 113 -TTTEQPKPMVOTKGRPHSQCLNSSPLS-HAQLMFPAPSPASARSVP-----DISKHR 165
QY 1006 LGGFTICRTIPASPOQKRFSLQFHNCPENKDSKLSPTFTQSRPLPSSNHRPAPSRP 1065
DB 166 PQAIVPCKIPASPOQKRFSLQFHNCPENKDSKLSPTFTQSRPSSNHRPAPSRP 225
QY 1066 TPGNTSKGDPKSNMTLTLNSSKCDSPGSSNSNAVIPSDETVFPVEEKCRLDVN 1125
DB 226 VEGSTKLDATKSSMTLGLGASRCDDSPGGGNSGNMAYIPDETVFTVEDKCRLDVN 285
QY 1126 TELNSSIEDLLEASMPSSDTVTYFKSEVAVLSPEKAENDTYKDYDNHNOCKEKEAE 1185
DB 286 TELNSSIEDLLEASMPSSDTVTYFKSEVAVLSPEKAENDTYKDYDNHNOCKEKEAE 345
QY 1186 EELALATAMMASODALPIVPOQVNGEDITIIODTPETLFGHTKAKQPIREDEWKL 1245
DB 346 EELALATAMMASODALPIVPOQVNGEDITIIODTPETLFGHTKAKQPIREDEWKL 405
QY 1246 GOQIGLGAESQOQADVGTGLMAVKQTYVNTSSQEEVEYEALERETRMASHLNHPN 1305
DB 406 GOQIGLGAESQOQADVGTGLMAVKQTYVNTSSQEEVEYEALERETRMASHLNHPN 465
QY 1306 IIRMLGATCEKSNYLFIFEMAGSVAHLLSKYGAPEKESVINYTBQLRLGSLYHENQI 1365
DB 466 IIRMLGATCEKSNYLFIFEMAGSVAHLLSKYGAPEKESVINYTBQLRLGSLYHENQI 525
QY 1366 IIRHDVGAULTDSTGQRIRIADFGAARLASGTGAGEFQGLCTIAFMAPEVLRGQO 1425
DB 526 IIRHDVGAULTDSTGQRIRIADFGAARLASGTGAGEFQGLCTIAFMAPEVLRGQO 585
QY 1426 YGRSCDWSVGALLIEMACAKPPWNAEKSHNLIFKIASATTAPISPSHLSPLGRDVA 1485
DB 586 YGRSCDWSVGALLIEMACAKPPWNAEKSHNLIFKIASATTAPISPSHLSPLGRDVA 645
QY 1486 LKCLELQPODRPPRELKHPVFRTTW 1512
DB 646 VKCLELQPODRPPRELKHPVFRTTW 672

RESULT 10

US-08-472-934-6
; Sequence 6, Application US/08472934
; Patent No. 5753446
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Iahive and Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,934
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/440,421
FILING DATE: 15-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/354,516
FILING DATE: 21-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 5,405,941
FILING DATE: 15-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/323,460
FILING DATE: 14-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. Decontili, Jr. Esq.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: CPT-004DVC02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 626 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-472-934-6

Query Match 7.1%; Score 559; DB 1; Length 626;
Best Local Similarity 29.9%; Pred. No. 1,8e-28;
Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOQKRFSLQFHNCPENKDSKLSPTFTQSRPLPSSN-----IHRPK----- 1062
DB 110 SSMKSLRILILLSQDN---HTSSPHSGVSRQVRIKPGSAGDITIIQAPPRRHLIS 166
QY 1063 -----SRPPPG-----NTSKGDPKSNMTLGLNSSKCDSPGSSNSNAVIP 1107
DB 167 VSSQNPGRSSPPGYVPERQOHAROG-----SYT-----SINSEGEFIP 206
QY 1108 SDETFTPEEKCRLDVNTLELNSIEDLLEASMPSSDTVTYFKSEVAVLSP----- 1158
DB 207 E-----YSEQMLDPLLSAENSLSGSCSLDRSADSPFRKSQSRARSFPDNRKES 259
QY 1159 -----EKAENDTY-----KDYVNHNOCKEKEAEDEEALAI---AMAMASQ 1199
DB 260 DRETQLYDKGVKGTYPRRYHVSVHHKQVNDGRTRTPRIRHOGNFTLVPPSRSLSTNG 319
QY 1200 DALPIVPO-----LOVNGEDITIIQODTPETLFGHTKAKQPIREDEWKLKGOQIGL 1252
DB 320 ENNGVAVOYLDPRGRLSADSENAITVOERNVPT-----KSP-SAPIMWRGKLGG 371
QY 1253 AFSSCYQADVGTGLMAVKQTYVNTSSQEEVEYEALERETRMASHLNHPRIIMGLA 1312
DB 372 AFGRYVLYCYDVTGRELAKSOVOFPDP-SPEYSKEVSALECEIQLKLNQHERIVQYYGC 430
QY 1313 TCEKSN--YNLFEMAGSVAHLLSKYGAPEKESVINYTBQLRLGSLYHENQIHRDVP 1370
DB 431 LNRBAEKILITMEYMPGSGVNDQKLKAYGALTESVYRKTRTROLEMSYLIHSMYIHRDI 490
QY 1371 KCANLLIDSTGQRIRIADFGAARLAS---KGTGAGEFQGLCTIAFMAPEVLRGQOYGV 1427

DB 491 KGANILRDSAG-NVKLDFGASKRLQITCMSTGI-----RSVGTGTPYMSPEVYISGSGYG 545
QY 1428 RSCDVMSVGCATITMACAKPPMNAEKHSNHLALIFKIASATTAPISPSHLSPLGLRDVALR 1487
DB 546 RKADVMSIGCTVEMLETKEPW-AEYEA--MAAIFKATQPTNPQLPSHISEGRDE-LR 601
QY 1488 CLELOPDDPPSRELLKH 1505
DB 602 RIFVEARORPSAEELLTH 619
RESULT 11
US-08-323-460A-6
Sequence 6, Application US/08323460A
Patent No. 5854043
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
RESPONSE TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS & MCINTOSH
STREET: 1700 LINCOLN STREET, SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,460A
FILING DATE: 14-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 626 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-460A-6
Query Match 7.1%; Score 559; DB 2; Length 626;
Best Local Similarity 29.9%; Pred. No. 1.8e-28;
Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

DB 260 DREQLYDKGVGGTYRRYRVSHHKKDYNDGRTPPRIRRHOGNLTFLVPSRSNSTNG 319
QY 1200 DALPVPQ-----LQVNGEDIIIIQODTPETLPGHFRAKOPYREDTEMLKGOQIGL 1252
DB 320 ENMGVAQYIDPDRRLSADSENALTYQERNVPI-----KSP-SAPIMMRBCKLLGOG 371
QY 1253 AFSSCYQADYVGTCTLMAVQVYVNRNTSSQEEVEALREIRMSHNLNPNIRMLGA 1312
DB 372 AFRVYLYCYVDYDGERELASKVOFPDP-SPEYSKREVSALBEIOLLNKHRIYQYCC 430
QY 1313 TCESN--YNTFTMAGSVAHLLSKYAFKESVYINTFQILRGISYHENQIIRDY 1370
DB 431 LRDRAEKILTFEMTEMGSKYKQDLKATGALTESVTRKTKOLLEGMSYLSHNMIVRDI 490
QY 1371 KGANILRDSAG-NVKLDFGASKRLQITCMSTGI-----RSVGTGTPYMSPEVYISGSGYG 545
DB 491 KGANILRDSAG-NVKLDFGASKRLQITCMSTGI-----RSVGTGTPYMSPEVYISGSGYG 545
QY 1428 RSCDVMSVGCATITMACAKPPMNAEKHSNHLALIFKIASATTAPISPSHLSPLGLRDVALR 1487
DB 546 RKADVMSIGCTVEMLETKEPW-AEYEA--MAAIFKATQPTNPQLPSHISEGRDE-LR 601
QY 1488 CLELOPDDPPSRELLKH 1505
DB 602 RIFVEARORPSAEELLTH 619
RESULT 12
US-08-461-146C-6
Sequence 6, Application US/08461146C
Patent No. 5981265
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHODS FOR REGULATING MEK PROTEIN ACTIVITY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,146C
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-004CN3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 626 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-146C-6

Query Match 7.1%; Score 559; DB 2; Length 626;
Best Local Similarity 29.9%; Pred. No. 1.8e-28;
Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOTQRFKSLQFHRCNCPKNDKSLSPVFTQSRPLPSSN-----IHRKP----- 1062
DB 110 SSSMKSLRILLLSQDRN---HTSSPHSGVSRQVRIRKPSQAGDINTITYQAPRGRHLS 166
QY 1063 -----SRPTPG-----HTSKGDPKSKSMITDLNSSKCDKDFSCSSNSSNAVIP 1107
DB 167 VSSQNGRSPPGYPERQOHAROG-----SYT-----SINSEGEFTIP 206
QY 1108 SDEVTFTPEEKCRLDVNTLNSIEDLLKASMPSSDTVTPEKSEVAVLSP----- 1158
DB 207 E-----TSEQCMDPLSSAENSLSGSCSLDRSADSPSFRKSQMSRARSPDNKECS 259
QY 1159 -----EKAENDDTY-----KDVNHNQCKEKEAEDEEALAI---AMASASQ 1199
DB 260 DRETQLYDKGVKGYPRRYHVSVHHKDYNDGKRTPPRIRRHQGNLFTLVPSRSLSSTNG 319
QY 1200 DALPIVQ-----LQVNGEDIIITQDTPETLPGHTRAKOPYREDEWMLKGOQIGG 1252
DB 320 ENMGVAVOYLDPRGRRLRSADSENALTVOERNPT-----KSP-SAPINMRGKLLGG 371
QY 1253 AFSSCYQADVGSTGLMAVKQVTVYVNTSSQEEVEVALREIRMSHNLHNPNIIRMLGA 1312
DB 372 AGRVYLYCYDVTGRELAKQVOFPDP-SPEYSKEVSALECEIQLKNIQHRIYQYGC 430
QY 1313 TCEKSN--YNLFEMWAGSVVAHLKSKYAFKESVYINTTEQLRLSLYHENOIIRHY 1370
DB 431 LRDRAEKILITFMEYVPGSVKQDLKAYGALTESVTRKTYRQLLEKMSVLSHNMIVHRI 490
QY 1371 KGANLLIDSTGORLRADGAARLAS---KGTAGEFQGLGTLTAFAPEVYLKGOQYG 1427
DB 491 KGANILRDSAG-NVXLGDPGASKRLQTCMSGTGI-----RSYTGTPYMWSPVYISGEYG 545
QY 1428 RSCDVWSVCALITEMACAPPMNAEKSHNLALIFKIASATTAAPSPISHLSPGLRDVALR 1487
DB 546 RKAQWVSLGCTVVEMLTEKPPM-AEYEA--MAAIFKIAIOTPINPOLPSHISEGRDP-LR 601
QY 1488 CLELQPDQRPSPRELK 1505
DB 602 RIFVEAKORPSAEELLTH 619

RESULT 13
US-08-461-145C-6
Sequence 6, Application US/08461145C
Patent No. 6074861
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: NOVEL MEK PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahnive and Cockfield, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.145C
FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CPT-004CNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 626 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-145C-6

Query Match 7.1%; Score 559; DB 3; Length 626;
Best Local Similarity 29.9%; Pred. No. 1.8e-28;
Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOTQRFKSLQFHRCNCPKNDKSLSPVFTQSRPLPSSN-----IHRKP----- 1062
DB 110 SSSMKSLRILLLSQDRN---HTSSPHSGVSRQVRIRKPSQAGDINTITYQAPRGRHLS 166
QY 1063 -----SRPTPG-----HTSKGDPKSKSMITDLNSSKCDKDFSCSSNSSNAVIP 1107
DB 167 VSSQNGRSPPGYPERQOHAROG-----SYT-----SINSEGEFTIP 206
QY 1108 SDEVTFTPEEKCRLDVNTLNSIEDLLKASMPSSDTVTPEKSEVAVLSP----- 1158
DB 207 E-----TSEQCMDPLSSAENSLSGSCSLDRSADSPSFRKSQMSRARSPDNKECS 259
QY 1159 -----EKAENDDTY-----KDVNHNQCKEKEAEDEEALAI---AMASASQ 1199
DB 260 DRETQLYDKGVKGYPRRYHVSVHHKDYNDGKRTPPRIRRHQGNLFTLVPSRSLSSTNG 319
QY 1200 DALPIVQ-----LQVNGEDIIITQDTPETLPGHTRAKOPYREDEWMLKGOQIGG 1252
DB 320 ENMGVAVOYLDPRGRRLRSADSENALTVOERNPT-----KSP-SAPINMRGKLLGG 371
QY 1253 AFSSCYQADVGSTGLMAVKQVTVYVNTSSQEEVEVALREIRMSHNLHNPNIIRMLGA 1312
DB 372 AGRVYLYCYDVTGRELAKQVOFPDP-SPEYSKEVSALECEIQLKNIQHRIYQYGC 430
QY 1313 TCEKSN--YNLFEMWAGSVVAHLKSKYAFKESVYINTTEQLRLSLYHENOIIRHY 1370
DB 431 LRDRAEKILITFMEYVPGSVKQDLKAYGALTESVTRKTYRQLLEKMSVLSHNMIVHRI 490
QY 1371 KGANLLIDSTGORLRADGAARLAS---KGTAGEFQGLGTLTAFAPEVYLKGOQYG 1427
DB 491 KGANILRDSAG-NVXLGDPGASKRLQTCMSGTGI-----RSYTGTPYMWSPVYISGEYG 545
QY 1428 RSCDVWSVCALITEMACAPPMNAEKSHNLALIFKIASATTAAPSPISHLSPGLRDVALR 1487
DB 546 RKAQWVSLGCTVVEMLTEKPPM-AEYEA--MAAIFKIAIOTPINPOLPSHISEGRDP-LR 601

QY 1488 CLELQPODRPPSRELLKH 1505
Db 602 RIFVEARORPSAEELTH 619

RESULT 14

US-09-423-890-12
; Sequence 12, Application US/09423890
; Patent No. 6312934
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
; FILE REFERENCE: CPI-085CPC
; CURRENT APPLICATION NUMBER: US/09/423,890
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: USSN 60/078,153
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: USSN 60/099,165
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 12
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-423-890-12

Query Match 7.1%; Score 559; DB 4; Length 626;
Best Local Similarity 29.9%; Pred. No. 1.8e-28;

Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOTOKRKSLOPHRNCPEKKDSDKLSPVFTQSRLPSSN-----IHRKP----- 1062
Db 110 SSSMKSLRILLSDRN---HTSSPHSGVSKQVIRKPSQSGAGDINTYQAPERSRLS 166
QY 1063 -----SRPTPG-----NTSKQDPSKNSMTLDINSSKDDSGCNSNSNAVIP 1107
Db 167 VSSQNPGRSSPPGVPYPERQOHIARQ-----SYT-----SINSGEPTP 206
QY 1108 SDEIVFTVEKCRLDVNTLSSIEDLEASMPSSDTTFFKSEVAVLSP----- 1158
Db 207 E-----TSQCMLDPLLSAENSLSGSCQSLDRSADSPFRKSQMSARSFPDRKECS 259
QY 1159 -----EKAENDPY-----KDVNNHOKCKEKEAEDEEALAI---AMAMSAQ 1199
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QY 1200 DALPIVPO-----LOVENGEDIIIIQODTPETLPHTKAKOPYREDTEMLKGOQIGLG 1252
Db 320 ENMGVAOVYLDPRGRRLRSADSENALTVOERNVPT-----KSP-SAPINNRGKLLGOG 371
QY 1253 AFSSCYAOADVGTGLMAVKNQVTVYRNTSSQOEVEVEALREIRMSHLNPNITRMIGA 1312
Db 372 AFGVNYLCYDVTGRELASKOVQFDPD-SPTSKESVSALEEDIDLKMLQHERIVQYGC 430
QY 1313 TCESKN--YNLFIEWMAAGSVAHLISKYGAFKESVINVYTBQLRGLSYLHENQIHRDV 1370
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QY 1371 KGANLLIDSTQGLRIADFGAARLAS---KGTGAGEFGOLLGTIAFMAEVLRGQOYG 1427
Db 491 KGANILIRDSAG-NVYLDGFGASKRLQITICMSGTGI---RSVGTGPYMSPEVVISGEGYG 545
QY 1428 RSCVWSGCAIIEMACAKPPMNAEKSHNLALIFKIASATTAIPSHLSPLGRDVALR 1487
Db 546 KKADWMSIGCTVVEMLTEKPPW-AEYEA--MAAIFKIAOTPTNPOLPSHISEHGRDF-LR 601
QY 1488 CLELQPODRPPSRELLKH 1505
Db 602 RIFVEARORPSAEELTH 619

RESULT 15

US-08-628-829-10
; Sequence 10, Application US/08628829A
; Patent No. 6333170
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To Exter
; FILE REFERENCE: CPI-004DPC3
; CURRENT APPLICATION NUMBER: US/08/628,829A
; PRIOR FILING DATE: 1996-04-05
; EARLIER APPLICATION NUMBER: 08/440,421
; EARLIER FILING DATE: 1995-05-15
; EARLIER APPLICATION NUMBER: 08/323,460
; EARLIER FILING DATE: 1994-10-14
; EARLIER APPLICATION NUMBER: 08/049,254
; EARLIER FILING DATE: 1993-05-15
; EARLIER APPLICATION NUMBER: 08/410,602
; EARLIER FILING DATE: 1995-04-24
; EARLIER APPLICATION NUMBER: 08/472,934
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-628-829-10

Query Match 7.1%; Score 559; DB 4; Length 626;
Best Local Similarity 29.9%; Pred. No. 1.8e-28;

Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOTOKRKSLOPHRNCPEKKDSDKLSPVFTQSRLPSSN-----IHRKP----- 1062
Db 110 SSSMKSLRILLSDRN---HTSSPHSGVSKQVIRKPSQSGAGDINTYQAPERSRLS 166
QY 1063 -----SRPTPG-----NTSKQDPSKNSMTLDINSSKDDSGCNSNSNAVIP 1107
Db 167 VSSQNPGRSSPPGVPYPERQOHIARQ-----SYT-----SINSGEPTP 206
QY 1108 SDEIVFTVEKCRLDVNTLSSIEDLEASMPSSDTTFFKSEVAVLSP----- 1158
Db 207 E-----TSQCMLDPLLSAENSLSGSCQSLDRSADSPFRKSQMSARSFPDRKECS 259
QY 1159 -----EKAENDPY-----KDVNNHOKCKEKEAEDEEALAI---AMAMSAQ 1199
Db 260 DRETQLYDKGVKGGTYPRRYVSVHHKDYNGKRTFFPIRHQGNLFTLVSSSLSTNG 319
QY 1200 DALPIVPO-----LOVENGEDIIIIQODTPETLPHTKAKOPYREDTEMLKGOQIGLG 1252
Db 320 ENMGVAOVYLDPRGRRLRSADSENALTVOERNVPT-----KSP-SAPINNRGKLLGOG 371
QY 1253 AFSSCYAOADVGTGLMAVKNQVTVYRNTSSQOEVEVEALREIRMSHLNPNITRMIGA 1312
Db 372 AFGVNYLCYDVTGRELASKOVQFDPD-SPTSKESVSALEEDIDLKMLQHERIVQYGC 430
QY 1313 TCESKN--YNLFIEWMAAGSVAHLISKYGAFKESVINVYTBQLRGLSYLHENQIHRDV 1370
Db 431 LRDRAREKLTITFMEYMPGGSVKDQLKAYGALTESVTRKTYQIQLGMSYLSNMTIVHDI 490
QY 1371 KGANLLIDSTQGLRIADFGAARLAS---KGTGAGEFGOLLGTIAFMAEVLRGQOYG 1427
Db 491 KGANILIRDSAG-NVYLDGFGASKRLQITICMSGTGI---RSVGTGPYMSPEVVISGEGYG 545
QY 1428 RSCVWSGCAIIEMACAKPPMNAEKSHNLALIFKIASATTAIPSHLSPLGRDVALR 1487
Db 546 KKADWMSIGCTVVEMLTEKPPW-AEYEA--MAAIFKIAOTPTNPOLPSHISEHGRDF-LR 601
QY 1488 CLELQPODRPPSRELLKH 1505
Db 602 RIFVEARORPSAEELTH 619

Search completed: December 20, 2002, 16:23:31
Job time : 41 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:40 ; Search time 52 Seconds

(without alignments)
3874.518 Million cell updates/sec

Title: US-09-697-898-2

Perfect score: 7825
Sequence: 1 MAAAGNRASSSGFPEARAT.....PDRPPRELLHPRFTTW 1512

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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2: /SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7515	96.0	1495	22	ABG04377
2	7515	96.0	1495	22	ABG04377
3	7515	96.0	1495	23	AA680291
4	6912.5	88.3	1493	20	AA142107
5	6912.5	88.3	1493	20	AA126234
6	6867	88.1	1375	23	AA601872
7	6867	85.2	1593	23	AA648935
8	6318.5	80.7	1302	20	AA42104
9	6318.5	80.7	1302	20	AA42104
10	3102.5	39.6	672	15	AA66029

11	3102.5	39.6	672	19	AA656157	A murine mtogen-a
12	3102.5	39.6	672	20	AA473318	Mitogen ERK kinase
13	3102.5	39.6	672	20	AA473536	MEKK1 protein. Mu
14	3102.5	39.6	672	21	AA601216	Murine MEKK1. Mus
15	3102.5	39.6	672	23	AA648934	Murine MEKK1-1. M
16	3098.5	39.6	672	16	AA677544	MEKK1 protein. Mu
17	2475.5	31.6	649	22	ABG04376	Novel human diagno
18	595.5	7.6	650	14	AA40974	STE11 protein phos
19	595.5	7.6	690	21	AA470101	Tobacco MAP kinase
20	587.5	7.5	642	21	AA470099	A. thaliana MAP ki
21	578	7.4	651	21	AA477941	A. thaliana enviro
22	578	7.4	651	21	AA470100	A. thaliana MAP ki
23	576	7.4	661	21	AA470098	A. thaliana MAP ki
24	559	7.1	626	19	AA456159	A. thaliana MAP ki
25	559	7.1	626	20	AA456159	A. thaliana MAP ki
26	559	7.1	626	20	AA456159	A. thaliana MAP ki
27	559	7.1	626	20	AA456159	A. thaliana MAP ki
28	559	7.1	626	21	AA456159	A. thaliana MAP ki
29	559	7.1	626	21	AA456159	A. thaliana MAP ki
30	558.5	7.1	626	23	AA456159	A. thaliana MAP ki
31	557.5	7.1	626	21	AA456159	A. thaliana MAP ki
32	543	6.9	619	19	AA456159	A. thaliana MAP ki
33	543	6.9	619	20	AA456159	A. thaliana MAP ki
34	543	6.9	619	21	AA456159	A. thaliana MAP ki
35	543	6.9	619	23	AA456159	A. thaliana MAP ki
36	536.5	6.9	619	23	AA456159	A. thaliana MAP ki
37	534.5	6.8	626	20	AA456159	A. thaliana MAP ki
38	531	6.8	619	19	AA456159	A. thaliana MAP ki
39	531	6.8	619	20	AA456159	A. thaliana MAP ki
40	531	6.8	619	20	AA456159	A. thaliana MAP ki
41	531	6.8	619	20	AA456159	A. thaliana MAP ki
42	531	6.8	619	21	AA456159	A. thaliana MAP ki
43	531	6.8	619	23	AA456159	A. thaliana MAP ki
44	530	6.8	619	20	AA456159	A. thaliana MAP ki
45	529.5	6.8	423	22	AA456159	A. thaliana MAP ki

ALIGNMENTS

RESULT 1
ID ABG04377 standard; Protein: 1495 AA.
AC ABG04377;
XX
DF 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #4368.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCR-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
PA (HYSE-) HYSEQ IMC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS68564.
XX
PT New isolated polynucleotide and encoded polypeptides; useful in
PT diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20: SEQ ID No 34736; 103bp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1495 AA;

Query Match Best Local Similarity 96.0%; Score 7515; DB 22: Length 1495;

Matches 1461; Conservative 3; Mismatches 28; Indels 2; Gaps 2;

21 SEBAGGGGALKAASAPAAAGLREAGSGRERADWRROKRYSVELDOLPEOPL 80
2 SEBAGGGGALKAASAPAAAGLREAGSGRERADWRROKRYSVELDOLPEOPL 61
81 AASPAASSTSPSPADAAAGSGTGFQPAVPPHGAASGGAHLTESVAAPDSGASPPA 140
62 AASPAASSTSPSPADAAAGSGTGFQPAVPPHGAASGGAHLTESVAAPDSGASPPA 121
141 AEPGERAPAAEPSPAAAPAGREMEKKTGLHKMDDEPERMIREKATCMPMKHE 200
122 AEPGERAPAAEPSPAAAPAGREMEKKTGLHKMDDEPERMIREKATCMPMKHE 181
201 WERRNRGPPVYVKPIPVKGDSEMNHLAESPGEVQASASPASKGRSPSPGNSPSGR 260
182 WERRNRGPPVYVKPIPVKGDSEMNHLAESPGEVQASASPASKGRSPSPGNSPSGR 241
261 TVKSSPGVRRKRVSPVPPQSGRITPPRRAPSPDGFSPSPETNRVKKVRAALYLQ 320
242 TVKSSPGVRRKRVSPVPPQSGRITPPRRAPSPDGFSPSPETNRVKKVRAALYLQ 301
321 QIGPNSFLIGDSPDNKYVFYFIPQNSCARGTFCILHFLVRLVQLEPSPMLRKTL 380
302 QIGPNSFLIGDSPDNKYVFYFIPQNSCARGTFCILHFLVRLVQLEPSPMLRKTL 361
381 KNEVEESLEFQKYHRRSSRIKAPSRNTIQKFVSRMSNSHTLSSSTSTSSSENSIKDEE 440
362 KNEVEESLEFQKYHRRSSRIKAPSRNTIQKFVSRMSNSHTLSSSTSTSSSENSIKDEE 421
441 QMCPICLLGMDDESLTVCEDGCRNKLHHHMSIAEECRNRREPLICLCRSKRSRSHF 500
422 QMCPICLLGMDDESLTVCEDGCRNKLHHHMSIAEECRNRREPLICLCRSKRSRSHF 481
501 YSHETSPVDPSPSLRAAQOQTVQOQPLAGSRNOESNFTLHYGQOQPPAYKDLAEPW 560
482 YSHETSPVDPSPSLRAAQOQTVQOQPLAGSRNOESNFTLHYGQOQPPAYKDLAEPW 541
561 IOVFGEMLVGLFSRNWVRENAALRLSHDVSGALLANGESTGNSGSGSSPSGSGATS 620
542 IOVFGEMLVGLFSRNWVRENAALRLSHDVSGALLANGESTGNSGSGSSPSGSGATS 601

621 GSSQNTISGDVVEACCSVLVSWCADPVYVVAALKTLRALMYTPCHSLAEIRIKLQRL 680
602 GSSQNTISGDVVEACCSVLVSWCADPVYVVAALKTLRALMYTPCHSLAEIRIKLQRL 661
681 QPVVDITLVKCADANSTQSLSTLLECKGAGELAVGREITKAGSIGGVVAVLC 740
662 QPVVDITLVKCADANSTQSLSTLLECKGAGELAVGREITKAGSIGGVVAVLC 721
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722 ILGNQTESNMWELLRLCLIDRLLEFPFAEFPVHSTVDVSAEVEIRYKLLSLTF 781
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782 ALQSDINSHMWKLSRIYLSARVTVVPHVSKLEMLSVS-STHFTRRRLMAI 841
860 ADEVEIAEALQIGVEDTLQDQ-DSFLQASVPNNILETTEENSPCTVLETKGLCAT 918
842 ADEVEIAEALQIGVEDTLQDQ-DSFLQASVPNNILETTEENSPCTVLETKGLCAT 901
919 KLSASSEDISERLASISVGPSSSTTTTTEQPKPMVOTKGRPHSQCLNSPILSHSOL 978
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979 MEPALSTPSSSTPVPAGTATVSKHRLQGFIPCRIPASAPOTQKFSIQFHRCENKD 1038
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1099 SNSNAVIPSDETVEFTVPEKCRLDVNTLNSIEDILASMSPSDTTTFSEVAVLSP 1158
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1159 EKAENDTTKDDVNNHKKCKEKEAEBEALAIAMASASODALPIVPOLOVBNEDIII 1218
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1219 IOODPPELTGHTKAKOPYREDTEMLKGOQIGAFSSCYQADVGTGLMAVKOYTYVR 1278
1202 IOODPPELTGHTKAKOPYREDTEMLKGOQIGAFSSCYQADVGTGLMAVKOYTYVR 1261
1279 NTSSEQEEVEALREIRMSHNLNHNITRMLGATCEKSNYNLFITMAGGSVAHLISKY 1338
1262 NTSSEQEEVEALREIRMSHNLNHNITRMLGATCEKSNYNLFITMAGGSVAHLISKY 1321
1339 GAFKESVYINTYEQLLRGSLYHENOIHRDYKGANLLDSTGQRLRIDFGAAALASK 1398
1322 GAFKESVYINTYEQLLRGSLYHENOIHRDYKGANLLDSTGQRLRIDFGAAALASK 1381
1399 GTGAGEFQQLGTTAFMAPEVLRGOQYGRSCDVMSVGCATTEMACAKPMAEKHSNL 1458
1382 GTGAGEFQQLGTTAFMAPEVLRGOQYGRSCDVMSVGCATTEMACAKPMAEKHSNL 1441
1459 ALIFKIASATPAPISIPSHLSPGLRDVALRCLELPDRPSEBLKHPVETRW 1512
1442 ALIFKIASATPAPISIPSHLSPGLRDVALRCLELPDRPSEBLKHPVETRW 1495

RESULT 2
AAB60291
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XX AAB60291;
AC
XX
DT 06-Apr-2001 (first entry)
XX
DE Human MEK1.
XX
KW Human MEK1; mitogen-activated protein kinase kinase kinase 1;
MEK kinase 1; MAP/ERK kinase kinase 1; pro-apoptotic;

11/11-1572
catalytic
down owl

KM apoptosis signal regulation; programmed cell death;
KM serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
KM Jun N-terminal kinase/stress-activated protein kinase;
KM Bcl-2 substrate; NF-kappa-B-mediated transcription regulation;
KM expression inhibition; antisense therapy;
KM hyperproliferative disorder; cancer; inflammation.
XX
OS Homo sapiens.
XX
PN U56168950-B1.
XX
PD 02-JAN-2001.
XX
PE 23-JUL-1999; 9905-0359756.
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PR 23-JUL-1999; 9905-0359756.
XX
PA (ISIS-) ISIS PHARM INC.
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PI Monia BP, Cowseert LM, Gaarde W, Ward DT;
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XX WPI: 2001-122264/13.
DR N-PSDB: AAF27079.
XX
XX
PT New antisense compound targeting nucleic acid encoding human
PT mitogen activated protein kinase kinase 1 (MEK1), useful for treating
PT diseases or conditions associated with MEK1 expression, or preventing
PT inflammation or tumor formation -
XX
XX
PS Example 15; Column 42-52; 35pp; English.
XX
CC This sequence represents human MEK1. MEK1 (also known as mitogen-
CC activated protein kinase kinase kinase 1, MEK kinase 1 and MAP/ERK
CC kinase kinase 1) is a dual-specific serine/threonine kinase which
CC mediates cellular responses to mitogenic stimuli, being involved in
CC JNK/SAPK (Jun N-terminal kinase/stress-activated protein kinase) MAP
CC kinase cascades. MEK1 regulates signalling events associated with
CC apoptosis (programmed cell death) and NF-kappa-B, both of which have
CC been associated with the development of hyperproliferative disorders
CC such as cancer. Specifically, MEK1 lies directly downstream of Bcl-2
CC in an apoptotic signalling cascade, and plays a critical role in the
CC control of NF-kappa-B-mediated transcription at multiple points in the
CC apoptotic cascade. The invention relates to antisense oligonucleotides
CC targeted to the human MEK1 gene, which inhibit its expression. A series
CC of oligonucleotides (AAF27086-AAF27125) were designed to target different
CC regions of the human MEK1 RNA, and were analysed for their effect on
CC MEK1 mRNA levels by quantitative real-time PCR. The oligonucleotides of
CC the invention are useful for diagnosis, prevention and treatment of
CC conditions associated with MEK1 expression, such as inflammation, and
CC cancer and other hyperproliferative disorders.
XX
XX
SQ Sequence 1495 AA:
Query Match 96.0%; Score 7515; DB 22; Length 1495;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1461; Conservative 3; Mismatches 28; Indels 2; Gaps 2;
QY 21 SPEAGGGGAGLAKASSAPAAAGLLREAGSGGERADWRRLRKRVSYELDQLEQPLFL 80
DB 2 SPEAGGGGAGLAKASSAPAAAGLLREAGSGGERADWRRLRKRVSYELDQLEQPLFL 61
QY 81 AASPASTSTSPRPAAAGAGTGFOPVAVPPHGAASRGGAHLTESVAADSGASSPAA 140
DB 62 AASPASTSTSPRPAAAGAGTGFOPVAVPPHGAASRRGAHLTESVAADSGASSPAA 121
QY 141 AEPSEKAPAAEPSPAAAPAGREMEKNTLGLHKMDRPERMIREKLTATCPAMKHE 200
DB 122 AEPSEKAPAAEPSPAAAPAGREMEKNTLGLHKMDRPERMIREKLTATCPAMKHE 181
QY 201 WLERRNRGPPVVKPIPVKGDGSEMHLLAASPEVQASAPASPKGRSPSPGNSPSGR 260
DB 182 WLERRNRGPPVVKPIPVKGDGSEMHLLAASPEVQASAPASPKGRSPSPGNSPSGR 241

QY 261 TYKSRPGVRRKRKRVSPVPOSGRITPPRRAPSPDOFSYSPDETNRNRNKKVRAALYLLO 320
DB 242 TVKSSPPVRRKRKRVSPVPOSGRITPPRRAPSPDOFSYSPDETNRNRNKKVRAALYLLO 301
QY 321 QIGPSFLLIGDPSPNKRVFVIGPONCSGARTFCILHFWLRYFOLEPSPMLMRRTL 380
DB 302 QIGPSFLLIGDPSPNKRVFVIGPONCSGARTFCILHFWLRYFOLEPSPMLMRRTL 361
QY 381 KNEVESLFOKYHSRRSSRIKAPSRRNTLOKFVSRMSNHTLSSSTSTSSSENSIKDEE 440
DB 362 KNEVESLFOKYHSRRSSRIKAPSRRNTLOKFVSRMSNHTLSSSTSTSSSENSIKDEE 421
QY 441 QMCPICLLGMDEESLTYCEGCCRKLHHHCHMSIAEDCRRNREPLICLRKWRSHDF 500
DB 422 QMCPICLLGMDEESLTYCEGCCRKLHHHCHMSIAEDCRRNREPLICLRKWRSHDF 481
QY 501 YSHELSPVDSPLRAAOQOTVOOQPLAGSRNSENPNLTHVGTQOIPPAVKDLAEFW 560
DB 482 YSHELSPVDSPLRAAOQOTVOOQPLAGSRNSENPNLTHVGTQOIPPAVKDLAEFW 541
QY 561 IOVFGMELVGLFSRNMMVREMALERLSHDVSALLLNGESTGSGSSGSSPGGATS 620
DB 542 IOVFGMELVGLFSRNMMVREMALERLSHDVSALLLNGESTGSGSSGSSPGGATS 601
QY 621 GSSQTSISGDVVEACCSYLSWVCADPVYKVVYALKTLRAMLVYTPCHSLAERIKLQRL 680
DB 602 GSSQTSISGDVVEACCSYLSWVCADPVYKVVYALKTLRAMLVYTPCHSLAERIKLQRL 661
QY 681 QPVDTILVKKCADANSRTSOLSTLLELCGKQAGELAVGRELLKAGSIGGVYVYVNC 740
DB 662 QPVDTILVKKCADANSRTSOLSTLLELCGKQAGELAVGRELLKAGSIGGVYVYVNC 721
QY 741 ILGNOTESNNMOELLGRCLIDLRLLEFPAAEYPIVISTVSOAPVIRYKKLLSLTF 800
DB 722 ILGNOTESNNMOELLGRCLIDLRLLEFPAAEYPIVISTVSOAPVIRYKKLLSLTF 781
QY 801 ALOSTDNSHSMWKGKSRITVYSSARMTVTVPVFVSKLLMLSVSS-STHFTMRRLMAI 859
DB 782 ALOSTDNSHSMWKGKSRITVYSSARMTVTVPVFVSKLLMLSVSS-STHFTMRRLMAI 841
QY 860 ADEVEIAAIOGVVDTLDDGOO-DSFLQASVNNVLETTENSPECTVHLEKGTGLAT 918
DB 842 ADEVEIAAIOGVVDTLDDGOO-DSFLQASVNNVLETTENSPECTVHLEKGTGLAT 901
QY 919 KLSASSEDISERLASISVSPSSSTTTTTTTEQPKPMVOTGRPHSQCLNSSPSLHNSQL 978
DB 902 KLSASSEDISERLASISVSPSSSTTTTTTTEQPKPMVOTGRPHSQCLNSSPSLHNSQL 961
QY 979 MFPALSTPSSSTPSVPACTATDVSKHRLQGFIPCRIPASAPQOTQRKFSLOFHRNCPENKD 1038
DB 962 MFPALSTPSSSTPSVPACTATDVSKHRLQGFIPCRIPASAPQOTQRKFSLOFHRNCPENKD 1021
QY 1039 SDKLSPVFTQSRPLPSSNIHPRKPSRPTPGNTSKGDSKSNMTDLNSSSKCDSPSCS 1098
DB 1022 SDKLSPVFTQSRPLPSSNIHPRKPSRPTPGNTSKGDSKSNMTDLNSSSKCDSPSCS 1081
QY 1099 SNSSNAVIPSDIEVFTPEEKCRLDVNTELNSSIIDLEASPSFSDTIVTFKSEVAVLSP 1158
DB 1082 SNSSNAVIPSDIEVFTPEEKCRLDVNTELNSSIIDLEASPSFSDTIVTFKSEVAVLSP 1141
QY 1159 EKAENDDTYKDDVNNOCCKEMEKEEBAALAIAMASASODALPIYQLOVENGEDITI 1218
DB 1142 EKAENDDTYKDDVNNOCCKEMEKEEBAALAIAMASASODALPIYQLOVENGEDITI 1201
QY 1219 IOODPTELPGHTAKOYREDTEMLKGOQIGLGFSSCYAOADVGSTLMAVKQVTVR 1278
DB 1202 IOODPTELPGHTAKOYREDTEMLKGOQIGLGFSSCYAOADVGSTLMAVKQVTVR 1261
QY 1279 NTSSBOEEVVALREIEMSHLNPNTIRMGATCEKSNYNTLEFEMAGSVAILLSKY 1338
DB 1262 NTSSBOEEVVALREIEMSHLNPNTIRMGATCEKSNYNTLEFEMAGSVAILLSKY 1321
QY 1339 GAFKESVYINTTEQLRLGLSTLHENQIITHRDYKCANLLIDSTGQRLRIADFGAARLASK 1398

DB 1322 GAFKESVINYITQRLRGSLYHENDIIRHDVAGANLLIDSTQRLKIDFGAARLASK 1381
QY 1399 GTGAGFQGGQLGTTAFMAPEVLRGQOYGRSCDWSVGCALIMACAKPWNKEKSHNL 1458
DB 1382 GTGAGFQGGQLGTTAFMAPEVLRGQOYGRSCDWSVGCALIMACAKPWNKEKSHNL 1441
QY 1459 ALIFKIASATTAISTSHLSPGLRDVALRCLQEPQDRPPSRELLKHVFRRTW 1512
DB 1442 ALIFKIASATTAISTSHLSPGLRDVALRCLQEPQDRPPSRELLKHVFRRTW 1495

RESULT 3

AAG80184

ID AAG80184 standard. Protein; 1495 AA.

XX AAG80184;

DT 21-JAN-2002 (first entry)

DE Human MEK kinase MEK1 protein fragment.

XX Oncogene; c-raf-1; human; MEK1; MEK kinase; raf-binding; cytosolic;

KW mitogen activated and extracellular stimuli regulated kinase;

KW gene therapy; NF-KB suppression; tumour cell proliferation;

KW NF-KB-mediated signal cascade.

XX Homo sapiens.

XX WO200179501-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-DE01518.

XX 14-APR-2000; 2000DE-1020138.

XX (RAPP/) RAPP U R.

XX (WIRT/) WIRTH T.

XX RAPP UR, WIRTH T;

XX WPI; 2002-017617/02.

XX N-PSDB; AAT68699.

XX New nucleic acid encoding partial raf sequence, useful for identifying

XX potential anticancer agents

XX Disclosure: Fig 11b-d; 66pp; German.

XX This invention describes a novel nucleic acid (I) that: (i) encodes at

XX least one raf partial sequence containing a MEK1 (mitogen activated and

XX extracellular stimuli regulated (MEK) kinase) binding site; (ii) encodes

XX at least one partial sequence of MEK1 containing a raf binding site;

XX (iii) is a silent mutation of (i) or (ii); or (iv) hybridizes to

XX (i)-(iii). The products of the invention have cytosolic activity and can

XX be used for gene therapy. The products also suppress NF-KB activation

XX resulting in inhibition of tumour cell proliferation or transformation.

XX (I), or proteins/peptides encoded by them, are useful for identifying

XX compounds that block binding of raf to MEK1. These compounds, optionally

XX where expressed from gene therapy vectors, are useful in human or

XX veterinary medicine for treatment of tumors. Antisense sequences, or

XX ribozymes, that bind to (I) are used to inhibit MEK1 activation. Also

XX nucleic acid (I') encoding at least a part of raf (or its silent

XX mutations or hybridizing sequences) is used to examine interaction of

XX encoded proteins with activation of the NF-KB-mediated signal cascade and

XX to screen for inhibitors of cell transformation by raf-mediated

XX activation of NF-KB. This sequence represents the human MEK1 protein

XX described in the method of the invention.

XX Sequence 1495 AA;

Query Match 96.0%; Score 7515; DB 23; Length 1495;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1461; Conservative 3; Mismatches 28; Indels 2; Gaps 2;

QY 21 SPFAGGGGALAKASAPAAAGLLREAGSGRRADRRRLKVSVEYLDQLEPDLF 80
DB 2 SPFAGGGGALAKASAPAAAGLLREAGSGRRADRRRLKVSVEYLDQLEPDLF 61
QY 81 AASPPASSTSPSPEDADAAGSGTGFPVAVPPHGAASRGALHTESVAAPDSGASPPAA 140
DB 62 AASPPASSTSPSPEDADAAGSGTGFPVAVPPHGAASRGALHTESVAAPDSGASPPAA 121
QY 141 AEPGEKRAPAEPSPAAAPAGREMEKNTKGLKHKDDREEMIREKIKATCPMAKHE 200
DB 122 AEPGEKRAPAEPSPAAAPAGREMEKNTKGLKHKDDREEMIREKIKATCPMAKHE 181
QY 201 WLERRNRRCGPVYVKKPIPVKDGSEMHLLAESPEGEVQASAPASGRSPSGNSPSGR 260
DB 182 WLERRNRRCGPVYVKKPIPVKDGSEMHLLAESPEGEVQASAPASGRSPSGNSPSGR 241
QY 261 TVKSESPGVARRKRVSPVFGSGRTTPRRAPSPDGFSPYSPEETNRVNVKVRARLYLQ 320
DB 242 TVKSESPGVARRKRVSPVFGSGRTTPRRAPSPDGFSPYSPEETNRVNVKVRARLYLQ 301
QY 321 QIGPNSFLIGDSDPDNKKYRFTIGPNCSCARGTCIHLFPVLRVQLPSDMLRKTL 380
DB 302 QIGPNSFLIGDSDPDNKKYRFTIGPNCSCARGTCIHLFPVLRVQLPSDMLRKTL 361
QY 381 KNEVESLFQKYSRRSSRRKAPSRNTIOKFVRMSNSHTLSSSTSSSESIIDEDE 440
DB 362 KNEVESLFQKYSRRSSRRKAPSRNTIOKFVRMSNSHTLSSSTSSSESIIDEDE 421
QY 441 QMCPICLLGLMDESLTVCEDGCRNKLHHKCMSIAMEECRRNEPLICPLCRSKWRSHP 500
DB 422 QMCPICLLGLMDESLTVCEDGCRNKLHHKCMSIAMEECRRNEPLICPLCRSKWRSHP 481
QY 501 YSHELSSPVDSPLSLLAAQOQTYQOOPLAGSRNOSNENLHYGQOIPPAYKDLAEPM 560
DB 482 YSHELSSPVDSPLSLLAAQOQTYQOOPLAGSRNOSNENLHYGQOIPPAYKDLAEPM 541
QY 561 IOVFGMEIVGCLFESRMNNVREMLRRLSHDVSQALLANGESTGNSGSGSSPSGATS 620
DB 542 IOVFGMEIVGCLFESRMNNVREMLRRLSHDVSQALLANGESTGNSGSGSSPSGATS 601
QY 621 GSSQTSISGDVYBACCSVLSMWCADPVYKYVAALKTLRLAMLYTPCHSLAERIKLQRL 680
DB 602 GSSQTSISGDVYBACCSVLSMWCADPVYKYVAALKTLRLAMLYTPCHSLAERIKLQRL 661
QY 681 QPVVDITLVKCADANRTSGLSITLLELCCKGAGELAVGREILKAGSIGIGVDVYVLC 740
DB 662 QPVVDITLVKCADANRTSGLSITLLELCCKGAGELAVGREILKAGSIGIGVDVYVLC 721
QY 741 ILGNQESNNMOELLRLCLIDLLLEFPFAEFPHIVSTVDVSOAEVEIRYKLLSLTF 800
DB 722 ILGNQESNNMOELLRLCLIDLLLEFPFAEFPHIVSTVDVSOAEVEIRYKLLSLTF 781
QY 801 ALQSDINSHMWGLSRRIYLSARAVTVPHVFSKLEMLSVS-STETTRMRRLIMAI 859
DB 782 ALQSDINSHMWGLSRRIYLSARAVTVPHVFSKLEMLSVS-STETTRMRRLIMAI 841
QY 860 ADEVEIAEALQIGVEYLDGQO-DSFLQASVPNNYLETENNSPECTVHLKTKGCLCAT 918
DB 842 ADEVEIAEALQIGVEYLDGQO-DSFLQASVPNNYLETENNSPECTVHLKTKGCLCAT 901
QY 919 KLSASSEDISERLARSIVGSSSTTTTTEBPQRMVOTKGRPHOCINSSPLSHSOL 978
DB 902 KLSASSEDISERLARSIVGSSSTTTTTEBPQRMVOTKGRPHOCINSSPLSHSOL 961
QY 979 MPFALSTPSSSTPVPAGTATDVSKHRLQGTICRIPASPCQRFSLQFHNCENMD 1038
DB 962 MPFALSTPSSSTPVPAGTATDVSKHRLQGTICRIPASPCQRFSLQFHNCENMD 1021
QY 1039 SDKLSPVFTQSRPLPSSNTHRPKSRPTPGNTSKQGPSPKNSMTLDLNNSSKCDSDSGCS 1098


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Db      1022 SDKLSPTFTSRLPSSNINRPKPSRPTPGNTSKQGPSSKNSMTLDLNSSKCDSDSGLS 1081
Qy      1099 SNSNAVIPSEDEVTFPVPEEKCRIDVNTETLNSSTIEDLLEASMPSSDPTVTVEKSEVAVLSP 1158
Db      1082 SNSNCCYTSDETFVTFVEEKCRIDVNTETLNSSTIEDLLEASMPSSDPTVTVEKSEVAVLSP 1141
Qy      1159 EKABNDTTYDDVNNHOKCEKMEABEEBALAMAMASASODALPIYPOLOVENGEDITII 1218
Db      1142 EKABNDTTYDDVNNHOKCEKMEABEEBALAMAMASASODALPIYPOLOVENGEDITII 1201
Qy      1219 IODTPELTGHTKAKOPYEDPEMLKGOOIGLGAFFSCYOAOVGVGTLMAYVOYTVR 1278
Db      1202 IQDTPETLTGHTKAKOPYEDPEMLKGOOIGLGAFFSCYOAOVGVGTLMAYVOYTVR 1261
Qy      1279 NTSSEGEVEVEALREETIRMSHNLNHPNIIIMLGATCEKSNYNLFIEWMAGSVANHLISKY 1338
Db      1262 NTSSEGEVEVEALREETIRMSHNLNHPNIIIMLGATCEKSNYNLFIEWMAGSVANHLISKY 1321
Qy      1339 GAKRESVYVITTDQLRGLSLYHENQIIHRDYGKANLLIDSTGCRKIIDFGAARLASK 1398
Db      1322 GAKRESVYVITTDQLRGLSLYHENQIIHRDYGKANLLIDSTGCRKIIDFGAARLASK 1381
Qy      1399 GTGAGEFGQLLGTIAPMAPEVLRGOOYGRSCDVSVGCAIITEMACAKPPNNAEKHSNHL 1458
Db      1382 GTGAGEFGQLLGTIAPMAPEVLRGOOYGRSCDVSVGCAIITEMACAKPPNNAEKHSNHL 1441
Qy      1459 ALIFKIASATTAIPSIPSHLSPLGLRDVALRCLLEQPODRPSPRELLKHPVFRTTW 1512
Db      1442 ALIFKIASATTAIPSIPSHLSPLGLRDVALRCLLEQPODRPSPRELLKHPVFRTTW 1495

RESULT 4
AA42107
ID      AA42107 standard; Protein; 1493 AA.
XX
AC      AA42107;
XX
DT      09-DEC-1999 (first entry)
XX
DE      Murine MEK1 protein sequence.
XX
KW      MEK1; MEK3; mitogen-activated protein kinase; MAPK; ERK;
KW      extracellular regulated kinase; signal transduction; regulation;
KW      MAPK/ERK; MKK; MKK; inflammation; cellular proliferation;
KW      differentiation; development; cell death.
XX
OS      Mus musculus.
XX
PN      M09947666-A2.
XX
PD      23-SEP-1999.
XX
PF      15-MAR-1999; 99MO-US05556.
PR      16-MAR-1998; 98US-0078153.
PR      04-SEP-1998; 98US-0099165.
XX
PA      (CADU-) CADUS PHARM CORP.
PI      Johnson GL.
XX
DR      WPI; 1999-571843/48.
DR      N-PSDB; AA425072.
XX
PT      New human MEK1 polynucleotides and polypeptides, used for regulating
PT      signal transduction in cells -
XX
PS      Example 1; Fig 4; 159pp; English.
CC      The present sequence represents murine mitogen-activated protein kinase/
CC      extracellular response kinase (MAPK/ERK) kinase kinase (MEK1),
CC      specifically designated MEK1. The MEK1 proteins are used to modulate
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CC      and regulate signal transduction in cells, as well as for regulation of
CC      gene transcription in a cell encoding MEK1, where the cell is involved
CC      in inflammation, regulation of cellular proliferation and
CC      differentiation, regulation of development, regulation of cell death or
CC      regulation of inflammation. They are also used to prepare antibodies.
CC      MEK1 polynucleotides can be used to produce the protein recombinantly
CC      and as a source of probes and primers.
XX
SQ      Sequence 1493 AA;
Query Match 88.3%; Score 6912.5; DB 20; Length 1493;
Best local similarity 89.5%; Pred. No. 0;
Matches 1358; Conservative 47; Mismatches 82; Indels 31; Gaps 11;
Qy      1 MAAAGNRASSSGEPGARATSPEA---GGCGALAKASSAPAA-AAGLIREAGSGGREAD 56
Db      1 MAAAGNRASSSGEPGARATSPEA---GGCGALAKASSAPAA-AAGLIREAGSGGREAD 60
Qy      57 WRRQLKRVRSVEIDQLPEQPLFLAAASPPCSTSPSPDEPDAAGASRFQPAAGPPPG 115
Db      61 WRRHVRKRVRSVEIDQLPEQPLFLAAASPPCSTSPSPDEPDAAGASRFQPAAGPPPG 120
Qy      116 AASRGGAHLTRESVAAPDSGASPAAPGEPKRAPAAPSPPAAPAGREMEKKTLLKGLH 175
Db      121 AASRGGSIAELAAARDSGARSPPAGAP-----PS-AAAPSGRMEKKTLLKGLH 170
Qy      176 MDDRPEERMIKREKLCATCMAMKHEMLERRNRGCVVYVPIPVGDGSEMHLLAESPG 235
Db      171 MEDRPEERMIKREKLCATCMAMKHEMLERRNRGCVVYVPIPVGDGSEVNNLLAEPPGE 230
Qy      236 VQASNAASPASGKRSPPSGNSPGRTRYKSESPGVARRKVSVPPOSGRITPPRRAPSPDG 295
Db      231 GQAGSAAPAPKGRSPSPSGSPSGSVKPESPGVARRKVSVPPOSGRITPPRRAPSPDG 290
Qy      296 FSPYSPDEETNRVKKVMARLYLLOQIGPNPFLIGGDSPPDKRYVFTIGPONCSGARCPFC 355
Db      291 FSPYSPDEETNRVKKVMARLYLLOQIGPNPFLIGGDSPPDKRYVFTIGPONCSGARCPFC 350
Qy      356 IHLFVMLRVPLQLEPSPDMLMRKTLKNEVESLFPKYHRSRSSRIKASRYNTQKFSRM 415
Db      351 IHLFVMLRVPLQLEPSPDMLMRKTLKNEVESLFPKYHRSRSSRIKASRYNTQKFSRM 410
Qy      416 SNSHTLSSSTSTSSSENSIDEEQMCPTCLGLMDEESLTVCEDGRNKLHHKMSIW 475
Db      411 SNSHTLSSSTSTSSSENSIDEEQMCPTCLGLMDEESLTVCEDGRNKLHHKMSIW 470
Qy      476 AEECRNRNEPLICPLCRSKWRSHPDYSHLSPPVSPSLAAAOQTVQOQPIAGS--RRN 534
Db      471 AEECRNRNEPLICPLCRSKWRSHPDYSHLSPPVSPSLAAAOQTVQOQPIAGS--RRN 530
Qy      535 QESNENLTHYGTQOIIPAYKDLAEPWIOVFGMELVGCLEFSRMNVRREMAIRLSHDVSGA 594
Db      531 QESNENLTHYGTQOIIPAYKDLAEPWIOVFGMELVGCLEFSRMNVRREMAIRLSHDVSGA 590
Qy      595 LLLANGESTGNSGGSGSGSPGGATSGSSQTSISGDVVEACCSVLSMYACADPVYKYVAA 654
Db      591 LLLANGESTGNSGGSGSGSLGASGASGSSQPSISGDVVEACCSVLSMYACADPVYKYVAA 650
Qy      655 LKTLRAMLVYTPCHSLAERIKLRLOLPVVDITLVKCADANSRYSQSLISTYLELCKCKQA 714
Db      651 LKTLRAMLVYTPCHSLAERIKLRLOLPVVDITLVKCADANSRYSQSLISTYLELCKCKQA 710
Qy      715 GELAVGREILKAGSIGIGGVYVNLCLIGNOTESNNMOELGLRLCLIDRLLEFPAPFP 774
Db      711 GELAVGREILKAGSIGIGGVYVNLCLIGNOTESNNMOELGLRLCLIDRLLEFPAPFP 770
Qy      775 HIVSTDVSOAPEVETIRYKLLSLTFALQSDINSHSMYKLSRRTYSSARNTVTPHVF 834
Db      771 HIVSTDVSOAPEVETIRYKLLSLTFALQSDINSHSMYKLSRRTYSSARNTVTPHVF 830
Qy      835 SKLEMLSVSSSTHTTTRRRRLMAIADVEVIAEAIQIGVEPTLDGQDSFOQASVPNNYL 894
Db      831 SKLVYMLNAGSSTHTTTRRRRLMAIADVEVIAEAIQIGVEPTLDGQDS--LQAAVAPISCL 889
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QY 895 ETTENSPECTVHLEKTEGKGLCATKLSASSEDISERLASISVGPSSSTTTTTTTEQPKP 954
DB 890 ---ENSSLEHTVHREKTEGKGLSATRLSASSEDISDLAIVSGVGLPSS-----TTTEQPKP 941
QY 955 MVOTGRPHSQCINSSPLSHHSOLMPALSTPSSSPSPAGATVPAGVSKHRLQGFPCRI 1014
DB 942 AVOTGRPHSQCINSSPLS-HAOLMPAPASAPCSSAPSPV-----DISKHPQAFVPCXI 995
QY 1015 PSASPOTORKFSLQFHRCNCPENKDSKLSPVFTQSRNPSPSSNHRKPSRPTPGNTSKOG 1074
DB 996 PSASPOTORKFSLQFHRCNCPENKDSKLSPVFTQSRNPSPSSNHRKPSRPTPGNTSKOG 1055
QY 1075 DSKNSMTLDLSSSKCDSEFCSSSSNAVIPSDETVPPEBEKRLDYNTEINSLSD 1134
DB 1056 DATKSSMTLDLSSSKCDSEFCSSSSNAVIPSDETVPPEBEKRLDYNTEINSLSD 1115
QY 1135 LLEASWPSDDTVTFKSEVAVLSPKAEKDDTVKDDVNNOCCKEKEAEDEEALAIAMA 1194
DB 1116 LLEASWPSDDTVTFKSEVAVLSPKAEKDDTVKDDVNNOCCKEKEAEDEEALAIAMA 1175
QY 1195 MSASODALPIVLOLVENEDIIIIQODTPETLPCHTKAKOPYREDETEWLKGGQIGLGA 1254
DB 1176 MSASODALPIVLOLVENEDIIIIQODTPETLPCHTKAKOPYREDETEWLKGGQIGLGA 1235
QY 1255 SSCYQADVGTGTLAAVQVTVRNTSSQEEVEALREIRMSHLNHPNIIIRMLGATC 1314
DB 1236 SSCYQADVGTGTLAAVQVTVRNTSSQEEVEALREIRMSHLNHPNIIIRMLGATC 1295
QY 1315 EKSNNLFIEMMAGSVAAHLISKYGFKEFSVYINTEQLRGISYHEHOIIRHDKGAN 1374
DB 1296 EKSNNLFIEMMAGSVAAHLISKYGFKEFSVYINTEQLRGISYHEHOIIRHDKGAN 1355
QY 1375 LLIDSTGRLRIADFGAARLASKGTGAGEFGQLGTITAFNAPEVLRGQYGRSCDWS 1434
DB 1356 LLIDSTGRLRIADFGAARLASKGTGAGEFGQLGTITAFNAPEVLRGQYGRSCDWS 1415
QY 1435 VCCATTEMACAPPMNAEKSHNHLIFKIASATTAPSTIPSHLSPELRVYALRCLELQ 1494
DB 1416 VCCATTEMACAPPMNAEKSHNHLIFKIASATTAPSTIPSHLSPELRVYALRCLELQ 1475
QY 1495 DRPSPRELLKHPVFRTTW 1512
DB 1476 DRPSPRELLKHPVFRTTW 1493

RESULT 5
AAV26234
ID AAV26234 standard; Protein: 1493 AA.
XX
AC AAV26234;
XX
DT 03-NOV-1999 (first entry)
XX
DE Murine MEK1 protein.
XX
KW Murine Mitogen ERK kinase 1 protein; MEK1; protease;
KW extracellular signal regulated kinase; ERK; signal transduction pathway;
KW regulation; apoptosis; protein kinase; cleavage; caspase; antibody;
KW kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection;
KW immunoreactive; diagnostic; therapeutic assay; reagent; disorder;
KW aberrant modification; mis-regulation; mutation; MEK1 gene;
KW aberrant post-translational modification.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Cleavage-site 871..874
FT /note= "Protease-resistant form of MEK1 protein
FT 875..1493 generated by mutation at this site"
FT Active-site /label= Active fragment
FT /note= "Mediates apoptosis"

XX
PN WO941385-A1.
XX
PD 19-AUG-1999.
XX
XX
PF 12-FEB-1999; 99WO-US02974.
XX
PR 13-FEB-1998; 98US-0023130.
XX
XX (CADU-) CADUS PHARM CORP.
XX
PI Johnson GL.
XX
DR WPI; 1999-508649/42.
XX
DR N-PSDB; AAX80911.
PT A new mammalian serine-threonine protein kinase for treating
PT disorder characterized by aberration of the enzyme gene
PS Claim 9; Page 119-124; 149pp; English.
XX
XX The present sequence is a murine Mitogen ERK Kinase 1 (MEK1)
CC protein, which functions to integrate proteases and signal transduction
CC pathways involved in the regulation of apoptosis. It is a 196 kDa protein
CC kinase, which upon cleavage at Asp 871/874 by caspase generates a 91 kDa
CC kinase fragment that induces apoptosis and a 113 kDa NH2-terminal
CC fragment. Mutant MEK1 proteins that are resistant to cleavage by caspase
CC proteases and capable of inhibiting apoptosis can be produced by
CC substituting amino acid residues 871-874 with Alanine. MEK1 proteins and
CC antibodies immunoreactive with MEK1 proteins are used in diagnostic and
CC therapeutic assays and reagents for detecting and treating disorders
CC involving aberrant modification, mis-regulation or mutation of MEK1 gene
CC and aberrant post-translational modification of MEK1 protein.
SQ Sequence 1493 AA:

Query Match 88.3%; Score 6912.5; DB 20; Length 1493;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 1358; Conservative 47; Mismatches 82; Indels 31; Gaps 11;

QY 1 MAAAGNRASSSGFPGARATSPPEA---GGGGALAKASAPAA-AGLLEAGSGGERAD 56
DB 1 MAAAGDRASSSGFPGAAAAPAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
QY 57 WRRROLKRVSYELDQLPEQPLFL-AASPPASSTSPSPPEADAAAGSGTGFOVAVPPPHG 115
DB 61 WRRRHVKRVSYELDQLPEQPLFLAAASPPCSTSPSPPEADAAAGSFGFOVAVPPPHG 120
QY 116 AASRGCAHLTESVAAPDSCGASPAAPAEPEKRAPAEPEPAAAPAGREKNEKTEGLGLK 175
DB 121 AASRGSHSAELAAARDSCGASPAAPAEPEKRAPAEPEPAAAPAGREKNEKTEGLGLK 170
QY 176 MDDREPERMIREKLTATCAMPKHEWLERNNRRGPVYVPIPKVGGSGMNHLAEPGE 235
DB 171 MEDREPERMIREKLTATCAMPKHEWLERNNRRGPVYVPIPKVGGSGMNHLAEPGE 230
QY 236 VQASASPASKGRSPSPGNSPGRTVKSESPGVRRKRVSPVFOGRTTPRRAPSPDG 295
DB 231 GQASAPAPKGRSPSPGNSPGRTVKSESPGVRRKRVSPVFOGRTTPRRAPSPDG 290
QY 296 FSPYSPEETNNRVNKKMARLYLQOIGNSPLIGDSDDNKTVRYTIGQONSCAGTTC 355
DB 291 FSPYSPEETNNRVNKKMARLYLQOIGNSPLIGDSDDNKTVRYTIGQONSCAGTTC 350
QY 356 IHLFVMLRVFQLEPSPDMLMRTKLNFEVESLFQYHRSRSRIKAPRNITQKRVSM 415
DB 351 IHLFVMLRVFQLEPSPDMLMRTKLNFEVESLFQYHRSRSRIKAPRNITQKRVSM 410
QY 416 SNSHTLSSSTSTSSSENSIKDEEQMCPICLGLMDESLTYCEDGCRNKLHHHCMSIW 475
DB 411 SNSHTLSSSTSTSSSENSIKDEEQMCPICLGLMDESLTYCEDGCRNKLHHHCMSIW 470
QY 476 AECRRNRNRPCLPCLRKRWKSHDFYSHLSBPVDSPLRAAQOQTVQOOPLAGS-RRN 534

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471 AEECRARRREPLIPCLCKSKRRSHDFYSHELSFVESPASIAAQQPSPOOPAGSGORN 530
535 QESNFNLTHYGOOIPPAYKDLEPMIOVFMELVGLFGRNMNVREMARLRLSHDVG 594
531 QESSFNLTHTGTOIPSAKYADLEPMIOVFMELVGLFGRNMNVREMARLRLSHDVG 590
595 LILANGESTNGSGSGSSSGGATSGSSOTISGDVEACCSYLSNVCADPYKYVAA 654
591 LILANGESTNGSGSGSSSGGATSGSSOTISGDVEACCSYLSNVCADPYKYVAA 650
655 LKTLRAMLVYTPCHSLAERIKLRLQPVDTLLVKCADNSRISQISTILELCKGQA 714
651 LKTLRAMLVYTPCHSLAERIKLRLQPVDTLLVKCADNSRISQISTILELCKGQA 710
715 GELAVGREILKAGSIGIGVYVYLCITGNOTESNNQELGRLCLDRILLEPFAEYP 774
711 GELAVGREILKAGSIGIGVYVYLCITGNOTESNNQELGRLCLDRILLEPFAEYP 770
775 HAYSTDVSOAPEYRIKRLSLITFPALOSINDSHSNGKLSRIYLSARMTVTPHVF 834
771 HAYSTDVSOAPEYRIKRLSLITFPALOSINDSHSNGKLSRIYLSARMTVTPHVF 830
835 SKLEMLSVSSSTHTPMRRRLMAIDVEFLAIAIQGVDFLDGODSFLQASVPMNYL 894
831 SKLVYTMNASGSTHTFTRMRRLMAIDVEFLAIAIQGVDFLDGODSFLQASVPMNYL 889
895 ETTENSPECTVHLKTKGKLCATKLASSEDISERLASISVGPSSSTTTTTTTEQPK 954
890 ---ENSLHETVAREKTKGKLSATRLSASEDISDRLAGSVGLPSS-----TTTEQPK 941
955 MVOTKRGPHSQCINSSPLSHSOLMPALSTPSSSTPSPVAGTADVSKRLRGCFPCRI 1014
942 AVOTKRGPHSQCINSSPLSHSOLMPALSTPSSSTPSPVAGTADVSKRLRGCFPCRI 995
1015 PSASPTORKEFSLQPHRNCENKDSOKLSPYFOSRPLSPSNHRRPSPSGTNGNSKOG 1074
996 PSASPTORKEFSLQPHRNCENKDSOKLSPYFOSRPLSPSNHRRPSPSGTNGNSKOG 1055
1075 DPSKSNMTLDLNNSSKDDDFGSSNNAVIPSDETFTVEBECKRLDVNTEINSSIED 1134
1056 DATKSSMTLDLGSARCDSDFGGNGSNNAVIPSDETFTVEBECKRLDVNTEINSSIED 1115
1135 LLEASMPSSSTYTFKSEVAVLSPEKAENDTYKDVNNHOKCKEKEAEDEBALATAMA 1194
1116 LLEASMPSSSTYTFKSEVAVLSPEKAENDTYKDVNNHOKCKEKEAEDEBALATAMA 1175
1195 MSASODALPIVPOLOYENGEDIIIOODPPELT.PGHTKAKOPYREDEWEMLKGOIGIAR 1254
1176 MSASODALPIVPOLOYENGEDIIIOODPPELT.PGHTKAKOPYREDEWEMLKGOIGIAR 1235
1255 SSGCYQADVGTGTMAVKQYTYVRNTSSSEQEEVEALREERIRMMSHLNHNIIIRMLGATC 1314
1236 SSGCYQADVGTGTMAVKQYTYVRNTSSSEQEEVEALREERIRMMSHLNHNIIIRMLGATC 1295
1315 EKSNTYLFETIEMAGGSVAHLSTKYGAFKESVINYTEQLRGSLYHENQIHRDVGAN 1374
1296 EKSNTYLFETIEMAGGSVAHLSTKYGAFKESVINYTEQLRGSLYHENQIHRDVGAN 1355
1375 LLLDSTGORLRIADFGAARLASKGTGAGFEGOLGTFAMAPVYLRGOOYRSCDVM 1434
1356 LLLDSTGORLRIADFGAARLASKGTGAGFEGOLGTFAMAPVYLRGOOYRSCDVM 1415
1435 VGCAIEMACAPPMNAEKSHNLALIFKASATTAAPSIPSHSPGLRDVALCLELOPQ 1494
1416 VGCAIEMACAPPMNAEKSHNLALIFKASATTAAPSIPSHSPGLRDVALCLELOPQ 1475
1495 DRPPSRELLKHPYFRTTW 1512
1476 DRPPSRELLKHPYFRTTW 1493

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ABG01872
ID ABG01872 standard; Protein; 1375 AA.
AC ABG01872;
XX
DE 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #1863.
XX
KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSQ INC.
XX
PI Dmanac RT, Liu C, Tang YT.
XX
DR WPI: 2001-639362/73.
XX N-FSDB; AAS66059.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
PS Claim 20; SEQ ID No 32231; 103pp; English.
XX
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1375 AA:
XX
Query Match 88.1%; Score 6893; DB 22; Length 1375;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1343; Conservative 3; Mismatches 27; Indels 2; Gaps 2;
XX
XX
XX 47 AGSGGRADWRROLRKVASVELDQLPEQPLFLAASPPASSPSPDEPADAAGSGTG 106
XX 1 AGSGGRADWRROLRKVASVELDQLPEQPLFLAASPPASSPSPDEPADAAGSGTG 60
XX
XX 107 PVAVPPHGAASRGALHTFSVAAPDSGASSPAAEPGEKRAAPSPAAAGREME 166
XX 61 PVAVPPHGAASRGALHTFSVAAPDSGASSPAAEPGEKRAAPSPAAAGREME 120

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QY 57 -----WRROARKVSYELDQLPEQPLFLAASPASTSPSPEDADAGSTGTF 105
Db 162 GGGGTACKCGVMTSCRSSRS-----SSPPRRRAHLLPVAGAGRCGRS 207
QY 106 QPV---AVPPHGAASRGHAHLETESVAAPDGSASPAAAPGEGEKRAAPAEPPAAAGR 162
Db 208 ESLPARAGPPPPGASCGSHSALAAARDSGARSPAGAE-----PS-AAASGR 257
QY 163 EMENKETLKLGHKMDRDEERMIEREKLATCMPAMKHEMLERRNRGPPVVKPIPVKGDG 222
Db 258 EMEKETLKLGHKMDRDEERMIEREKLATCMPAMKHEMLERRNRGPPVVKPIPVKGDG 317
QY 223 SEMNHLAAEPGEVQAASAPASGRSPSPGNSPGRYAKSESPGVRKRRKRVSPVQSG 282
Db 318 SEVNNLAAEPGEVQAASAPASGRSPSPGNSPGRYAKSESPGVRKRRKRVSPVQSG 377
QY 283 RITPPRRAPSPDGFSPSPETNRNVRKVMARLYLLQOIGPNFLLGGSDPDKKRYFTI 342
Db 378 RITPPRRAPSPDGFSPSPETNRNVRKVMARLYLLQOIGPNFLLGGSDPDKKRYFTI 437
QY 343 GPONCSGARGTFCTHLLFVMLRVFQLEPSPMLMRKTLKNEVESLRFQYHSRRSRKA 402
Db 438 GPONCSGARGTFCTHLLFVMLRVFQLEPSPMLMRKTLKNEVESLRFQYHSRRSRKA 497
QY 403 PSRNTIOKFYSRMSNSTLSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 462
Db 498 PSRNTIOKFYSRMSNSTLSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 557
QY 463 CRNKLHHCHSINAECCRNRREPLICPLCRSKMSHDYFSEHLSPPVDSPLAAOQOT 522
Db 558 CRNKLHHCHSINAECCRNRREPLICPLCRSKMSHDYFSEHLSPPVDSPLAAOQOT 617
QY 523 VOOOPLAGS--RMOESNMLTHYGTQOIPPAYKDLEPMIOWFQEMELVGCLEFSNNMVR 581
Db 618 SPOOPVAGSQRRNOESFNLFHCTQOIPSAKYKDLEPMIOWFQEMELVGCLEFSNNMVR 677
QY 582 MALRLSHDVSGALLLANGESTGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 641
Db 678 MALRLSHDVSGALLLANGESTGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 737
QY 642 VCADPVYKVVVAALKTLRAMLVYTPCHSLAEIRIKLORLLOPVVTIIVKCADASRTSOL 701
Db 738 VCADPVYKVVVAALKTLRAMLVYTPCHSLAEIRIKLORLLOPVVTIIVKCADASRTSOL 797
QY 702 S1STLELCGQAGELAVGREILKAGSIGIGVDYVNCILIGNOTESNNMOELLGRCLLI 761
Db 798 S1STLELCGQAGELAVGREILKAGSIGIGVDYVNCILIGNOTESNNMOELLGRCLLI 857
QY 762 DRLLERPAEFYHIVTDSQAEPEIRIKKLSLITPALOSTDNGSHWYKLSRRIYL 821
Db 858 DRLLERPAEFYHIVTDSQAEPEIRIKKLSLITPALOSTDNGSHWYKLSRRIYL 917
QY 822 SSARMVTVVHVFSEKLEMLSVSSTFTFMRRLMAIADEVEIAEALIOGVEDTLGQOO 881
Db 918 SSARMVTVVHVFSEKLEMLSVSSTFTFMRRLMAIADEVEIAEALIOGVEDTLGQOO 977
QY 882 DSELOASVPNNYLETENESPECTVHLEKTKGLCATKLSASSEDISERLASISVGPSSS 941
Db 978 DS-LOAVAPTSCL---ENSLSEVHTREKTKGKLSATRLSASSSDISDRLAGVGLPSS 1033
QY 942 TTTTTTTEQPKPMVQTKGRPHSQCLNSPLSHSQMLPALSPSSSTSPVPGTATDV 1001
Db 1034 -----TTTEQPKPMVQTKGRPHSQCLNSPLSHSQMLPALSPSSSTSPVPGTATDV 1082
QY 1002 SKHRLQGFICRIIPASPOFORKFSLOFHRCNCPENKDSKLSPEVTSRPLPSSNIRPK 1061
Db 1083 SKHRLQGFICRIIPASPOFORKFSLOFHRCNCPENKDSKLSPEVTSRPLPSSNIRPK 1142
QY 1062 PSRPTPGNTSKQGDPSKNSMTLDLNSKCDSPGSCSSNSNAVIPSEDEVTFYFVEEKCR 1121
Db 1143 PSRVPSTSKLGDATKSSMTLDLGDASRCDSPGSCGNSGNNAVIPSEDEVTFYFVEEKCR 1202
QY 1122 LDVNTLELNSSTEDLEASMPSSDITVTFKSEVAVLSPKKAENDDTYKDDVNHNOCKCKEM 1161

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Db 1203 LDVNTLELNSSTEDLEASMPSSDITVTFKSEVAVLSPKKAENDDTYKDDVNHNOCKCKEM 1262
QY 1182 EAEFEELALAIAMASASODALPIVPOLOVENGEDIITIOODTPELTGHTRAKOPYREDT 1241
Db 1263 EAEFEELALAIAMASASODALPIVPOLOVENGEDIITIOODTPELTGHTRAKOPYREDT 1322
QY 1242 EWLKQOIGLGAFFSSCYQAOADVGTGTLMAVKQVTVYNTSSSEDEVEVALREIRMSHL 1301
Db 1323 EWLKQOIGLGAFFSSCYQAOADVGTGTLMAVKQVTVYNTSSSEDEVEVALREIRMSHL 1382
QY 1302 NHPNIIIMLGATCKESYNVLFIEEMAGSVAHLISKGAFRESYVINTEDLLGLSYLH 1361
Db 1383 NHPNIIIMLGATCKESYNVLFIEEMAGSVAHLISKGAFRESYVINTEDLLGLSYLH 1442
QY 1362 ENQIITHRDVKGANLLIDSTGRLRIADFGAARLASKGTGAGEGOLLGTIAPMADEVL 1421
Db 1443 ENQIITHRDVKGANLLIDSTGRLRIADFGAARLASKGTGAGEGOLLGTIAPMADEVL 1502
QY 1422 RGQOYGRSCDVWSYGCAIIEMACAKPPMNAEKHSNHLALIFKIASATTAPSIPLSLPGL 1481
Db 1503 RGQOYGRSCDVWSYGCAIIEMACAKPPMNAEKHSNHLALIFKIASATTAPSIPLSLPGL 1562
QY 1482 RDVALRCLEIOPDORPPSREILKHPVFRITW 1512
Db 1563 RDVALRCLEIOPDORPPSREILKHPVFRITW 1593

RESULT 8
AAV42104
ID AAV42104 standard; Protein: 1302 AA.
AC AAV42104;
DE 09-DEC-1999 (first entry)
XX
DE Human MEK1 protein sequence.
XX
KW MEK1; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK;
KW extracellular regulated kinase; signal transduction; regulation;
KW MAPK/ERK; MEK; MEKK; inflammation; cellular proliferation;
KW differentiation; development; cell death.
XX
OS Homo sapiens.
XX
PN WO947686-A2.
XX
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99WO-US05556.
XX
PR 16-MAR-1998; 98US-0078153.
PR 04-SEP-1998; 98US-0099165.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Johnson GL;
XX
PI WPI: 1999-571843/48.
XX
DR N-PSDB; AA225069.
XX
PT New human MEK polynucleotides and polypeptides, used for regulating
PT signal transduction in cells -
XX
PS Claim 12; Fig 2; 159pp; English.
XX
CC The present sequence represents human mitogen-activated protein kinase/
CC extracellular response kinase (MAPK/ERK) kinase kinase (MEKK),
CC specifically designated MEK1. The MEK proteins are used to modulate
CC and regulate signal transduction in cells, as well as for regulation of
CC gene transcription in a cell encoding MEK, where the cell is involved
CC in inflammation, regulation of cellular proliferation and
CC differentiation, regulation of development, regulation of cell death or

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CC regulation of inflammation. They are also used to prepare antibodies.
CC MEK polynucleotides can be used to produce the protein recombinantly
CC and as a source of probes and primers.

SQ Sequence 1302 AA;

Query Match	80.7%;	Score 6318.5;	DB 20;	Length 1302;
Post local similarity:	03.48;	Score 0;	DB 0;	Length 0;

Matches 1230; Conservative 26; Mismatches 46; Indels 15; Gaps 5;

QY	196	AMKHEMLERRRRRRRGVVYVKP.LPVYGDGS	EMNHLLAAESPGVEQOASAPASKGRSPSPGN	255
Db	1	AMKHEMLERRRRRRRGVVYKPLPVYKDGDS	EMNHLLAAESBGEVQOASAPASKGRSPSPGN	60
QY	256	SPSGRTVKSSES	PGVRRKRVSPVPOSGRTIPPRRASPDPGSPYSPEETNRNRVKKWRAR	315
Db	61	SPSGRTVKSSES	PGVRRKRVSPVPOSGRTIPPRRASPDPGSPYSPEETNRNRVKKWRAR	120
QY	316	LYLLOQITPNSFLIGGSDPDKKYVFTIGP	ONCSARGTFCIHLLFYMLRVPOLPSPDML	375
Db	121	LYLLOQITPNSFLIGGSDPDKKYRVFTIGP	ONCSARGTFCIHLLFYMLRVPOLPSPDML	180
QY	376	WRKTLKNEFEVSLFOKYSRSSRSRLKAPSRNT	IOKPFYSRMSNSTLSSSTSTSSNSNI	435
Db	181	WRKTLKNEFEVSLFOKYSRSSRSRLKAPSRNT	IOKPFYSRMSNSTLSSSTSTSSNSNI	240
QY	436	KDEEOMPCICLLGLMDDESJLVCE	DGCRNKLHHCHMSIABECCRNRREPLICPLCSKW	495
Db	241	KDEEOMPCICLLGLMDDESJLVCE	DGCRNKLHHCHMSIABECCRNRREPLICPLCSKW	300
QY	496	RSHDPYSHELSSPVDSPBSLSLAAOQOQY	QOQOPLAGSRRNDESNLTHTGTQOIPRAYKD	555
Db	301	RSHDPYSHELSSPVDSPBSLSLAAOQOQY	QOQOPLAGSRRNDESNLTHTGTQOIPRAYKD	360
QY	556	LAEPFIQVFGMELVGCLEFSRMMN	REMLRSLSDVSGALLIANGESTGSGSGSGSPS	615
Db	361	LAEPFIQVFGMELVGCLEFSRMMN	REMLRSLSDVSGALLIANGESTGSGSGSGSL	420
QY	616	GGATSGSSOTSISGDVVEACCSVL	SMYCADPVYKVVYAAALKTJLAMLVYTPCHSLAERIK	675
Db	421	AGASGSSQPSISGDVVEACCSVL	SIYCADPVYKVVYAAALKTJLAMLVYTPCHSLAERIK	480
QY	676	LQRLLOPVPYDITLVKCADAN	SRTOQLSITLLELCKQOAGELAVGREILKAGSIGICVD	735
Db	481	LQRLLRPVYDITLVKCADAN	SRTOQLSITLLELCKQOAGELAVGREILKAGSIGICVD	540
QY	736	YVLNCIICNOTESNNMWOEL	GLRCLDLRLLLEPFAEYEPHLYSTVDVQOAPVEIRYKXL	795
Db	541	YVLSCTICNOAESNNMWOEL	GLRCLDLRLLLEPFAEYEPHLYSTVDVQOAPVEIRYKXL	600
QY	796	SLLTFALQSIDNSHSMYKGLSR	RIYLSARAVYTVPVHFKLEMLSVSSSTHTFRMRR	855
Db	601	SLLTFALQSIDNSHSMYKGLSR	RIYLSARAVYTVPVHFKLEMLSVSSSTHTFRMRR	660
QY	856	LMALADEVELAEALIOGV	EDTLDGQODSFLQASVPNNYLETTESSSPECTVHLTEKTKGL	915
Db	661	LMALADEVELAEALIOGV	EDTLDGQODSFLQALAPACSL--ENSSLEHTVHREKTKGCL	716
QY	916	CATKLSASEDISERLMSIS	VGSPSSSTTTTTEETTEOKRPMYOKIKGRPHSOCLMSSPLSH	975
Db	717	SATRLSASSEDISIRLMSIS	VGSPSSSTTTTTEETTEOKRPMYOKIKGRPHSOCLMSSPLSH	770
QY	976	SQMLFPAISPSSSTSPV	YPACATADVSGKNHLOGEIPERIGASBPQOIRKSLQPHNRCPRE	1030
Db	826	HRSDOLSPVETQGRPPSS	NIHPRKPSRPVCGTSKLDGATKSSMTLDGASACDDSP	885
QY	1036	GCSNSNAVTPRSDYVFTY	PEEKSCRVDVNTELNLSITEDLLKASMPSSDTTVYFKSEVAY	115
Db	886	GGSNSNAVTPRSDYVFTY	PEEKSCRVDVNTELNLSITEDLLKASMPSSDTTVYFKSEVAY	945

QY	1156	LSEKAEANDDYIKDQVANHNOCKEKEKMEAEBEELALIAMMSASODALPIVPOLOYENED	1215
Db	946	LSPEAKENDDYIKDQVANHNOCKEKEKMEAEBEELALIAMMSASODALPIVPOLOYENED	1005
QY	1216	IIIIIOODPELPHGTAKAKOPYREDPEYMLKGQOIGAGFSSCYQADQDGTGTLIAWKVYT	1275
Db	1006	IIIIIOODPELPHGTAKAKOPYREDPEYMLKGQOIGAGFSSCYQADQDGTGTLIAWKVYT	1065
QY	1276	YVRNNTSBOEBEYVALKEEETIRMSHSHLNHPNIIIMLGATEKSNYMLFIEMMAGGSVALLL	1335
Db	1066	YVRNNTSBOEBEYVALKEEETIRMSHSHLNHPNIIIMLGATEKSNYMLFIEMMAGGSVALLL	1125
QY	1336	SKYGAFKESVYINTYEODLLRGSLYLHENQIIRHDVKGANLLIDSTGQRLIADFGAARL	1395
Db	1126	SKYGAFKESVYINTYEODLLRGSLYLHENQIIRHDVKGANLLIDSTGQRLIADFGAARL	1185
QY	1396	ASKGTGAGEFQGLGTLIAPMAPEYVLRGQOYGRSCDWSYVGCATTEMACAPPMNAEKHS	1455
Db	1186	ASKGTGAGEFQGLGTLIAPMAPEYVLRGQOYGRSCDWSYVGCATTEMACAPPMNAEKHS	1245
QY	1456	NHMLIFKIASATAPSPISHSISPLRDVALRCLTELQPODRPSPHELLKHPYFRITTY	1512
Db	1246	NHMLIFKIASATAPSPISHSISPLRDVALRCLTELQPODRPSPHELLKHPYFRITTY	1302

RESULT 9	
AAV26235	
ID	AAV26235 standard; Protein: 1302 AA.
XX	
AC	AAV26235;
XX	
DT	03-NOV-1999 (first entry)
XX	
DE	Human MEK1 protein.
XX	
KW	Human Mitogen ERK Kinase Kinase 1 protein; MEK1; protease;
KW	extracellular signal regulated kinase; ERK; signal transduction pathway
KW	regulation; apoptosis; protein kinase; cleavage; caspase; antibody;
KW	kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection
KW	immunoreactive; diagnostic; therapeutic assay; reagent; disorder;
KW	aberrant modification; mis-regulation; mutation; MEK1 gene;
KW	aberrant post-translational modification.
XX	
OS	Homo sapiens.
XX	
FH	
FT	Key
FT	Cleavage-site
FT	Location/Qualifiers
FT	681..684
FT	/note="Protease-resistant form of MEK1 protein
FT	generated by mutation at this site"
FT	685..1303
FT	/label="Active_fragments
FT	/note="Mediates apoptosis"
XX	
PN	W09941385-A1.
XX	
PD	19-AUG-1999.
XX	
PF	12-FEB-1999;
XX	99WO-US02974.
XX	
PR	13-FEB-1998;
XX	98US-0023130.
XX	
PA	(CADU-) CADUS PHARM CORP.
XX	
PI	Johnson GL;
XX	
DR	WPI: 1999-508649/42.
DR	N-PSDB; AAX80912.
XX	
PT	A new mammalian serine-threonine protein kinase for treating
PT	disorder characterized by aberration of the enzyme gene
XX	
PS	Claim 13; Page 130-134; 149pp; English.

XX The present sequence is a human Mitogen ERK kinase 1 (MEK1)
 CC protein, which functions to integrate proteases and signal transduction
 CC pathways involved in the regulation of apoptosis. It is a 196 kDa protein
 CC kinase, which upon cleavage at Asp 681/684 by caspase generates a 91 kDa
 CC kinase fragment that induces apoptosis and a 113 kDa NH2-terminal
 CC fragment. Mutant MEK1 proteins that are resistant to cleavage by caspase
 CC proteases and capable of inhibiting apoptosis can be produced by
 CC substituting amino acid residues 681-684 with Alanine. MEK1 proteins and
 CC antibodies immunoreactive with MEK1 proteins are used in diagnostic and
 CC therapeutic assays and reagents for detecting and treating disorders
 CC involving aberrant modification, mis-regulation or mutation of MEK1 gene
 CC and aberrant post-translational modification of MEK1 protein.
 XX
 SQ Sequence 1302 AA;
 Query Match 80.7%; Score 6318.5; DB 20; Length 1302;
 Best Local Similarity 93.4%; Pred. No. 0;
 Matches 1230; Conservative 26; Mismatches 46; Indels 15; Gaps 5;
 QY 196 AMKHEMLERRRRRCPPVVKPIPVKGDSEMMNHLAESPGEVQASAPASKGRSPSPGN 255
 DB 1 AMKHEMLERRRRRCPPVVKPIPVKGDSEMMNHLAESPGEVQASAPASKGRSPSPGN 60
 QY 256 SPSGRYKSSSPGVRKRVSPVPPQSGRIIPRRAPSPDGSPIYSPETNRKVKMAR 315
 DB 61 SPSGRYKSSSPGVRKRVSPVPPQSGRIIPRRAPSPDGSPIYSPETNRKVKMAR 120
 QY 316 LYLLOQIPNSFLIGDSPDKKRVFIFGPNQSCARGFCFHLFVMLRVYQLPSPDML 375
 DB 121 LYLLOQIPNSFLIGDSPDKKRVFIFGPNQSCARGFCFHLFVMLRVYQLPSPDML 180
 QY 376 WRKTLKNEVESLEFQKHSRRSRIRKAPSRNTLOKFVSRMSNHTLSSSTSTSSSENSI 435
 DB 181 WRKTLKNEVESLEFQKHSRRSRIRKAPSRNTLOKFVSRMSNHTLSSSTSTSSSENSI 240
 QY 436 KDEEEOKCPICLLGMDDEESTIYCEDECRNKLHHCHMSIYAEERRRRREPIICPLCRSKW 495
 DB 241 KDEEEOKCPICLLGMDDEESTIYCEDECRNKLHHCHMSIYAEERRRRREPIICPLCRSKW 300
 QY 496 RSHDFYSHEISSPYDSSSLRAAQOQTVQOQPLAGSRNDESNLTHYGOQIPPAYKD 555
 DB 301 RSHDFYSHEISSPYDSSSLRAAQOQTVQOQPLAGSRNDESNLTHYGOQIPPAYKD 360
 QY 556 LAEPMIOVFCMELVGLCFSRMNVREMLRLSHDVSGALLLANGESTGNSGGSGSSPS 615
 DB 361 LAEPMIOVFCMELVGLCFSRMNVREMLRLSHDVSGALLLANGESTGNSGGSGSSPS 420
 QY 616 GGATSGSSQTSISGDVYVACCSYLSMYCADPVYVYVAALKTLRAMLYTPCHSLAERIK 675
 DB 421 AGAASGSSQTSISGDVYVACCSYLSMYCADPVYVYVAALKTLRAMLYTPCHSLAERIK 480
 QY 676 LQRLLOPVVPTIIVKCADANSRTSOLSTLTLECKGOAGELAVGRELWAGSTIGIGVD 735
 DB 481 LQRLLOPVVPTIIVKCADANSRTSOLSTLTLECKGOAGELAVGRELWAGSTIGIGVD 540
 QY 736 YVINCILIGNOTESNMQELLGRCLLIDRLLEPFAEFYPHIVSTVDSQAEVEIRYKLL 795
 DB 541 YVINCILIGNOTESNMQELLGRCLLIDRLLEPFAEFYPHIVSTVDSQAEVEIRYKLL 600
 QY 796 SLTLFALQSDINSHSMGKLSRRIYLSARAVTVPHVFSKLEMLSVSSSTHTTRMRR 855
 DB 601 SLTLFALQSDINSHSMGKLSRRIYLSARAVTVPHVFSKLEMLSVSSSTHTTRMRR 660
 QY 856 LMAIADAEVEIAEATOLGVEPTLDGQODSPLOASVPNNVLETTENSPECTVHLEKTKGL 915
 DB 661 LMAIADAEVEIAEATOLGVEPTLDGQODSPLOASVPNNVLETTENSPECTVHLEKTKGL 716
 QY 916 CARLISASSEDISERLASISVGPSSSTTTTTLTEQPKPVQOTGRPHSOCLNSPLSH 975
 DB 717 SARLISASSEDISERLASISVGPSSSTTTTTLTEQPKPVQOTGRPHSOCLNSPLSH 770
 QY 976 SOLMFPALSTPSSSTPSPVAGTATDVSKHRLQGIPICRIPASAPQOTOKRKSLOPHRNCPE 1035

DB 771 AQLMFPAPASPCSSAPSV-----DISKHPQAVPCKIPASAPQOTOKRKSLOPHRNCPE 825
 QY 1036 NKDSDDKLSPVYTORRPPSSNIHRRKPSRPFGMTSKOGDPSKSMPLDINSSKCDSD 1095
 DB 826 HRSDQLSPVYTORRPPSSNIHRRKPSRPFGMTSKOGDPSKSMPLDINSSKCDSD 885
 QY 1096 GCSNNSNAVIPSDVETFTVPEEKCRLDVNTLSSIEDLLEASMPSSDFTVPEKSEVAV 1155
 DB 886 GCGGNSGNAVIPSDVETFTVPEEKCRLDVNTLSSIEDLLEASMPSSDFTVPEKSEVAV 945
 QY 1156 LSPKAEKNDTYKDDVHNOKCKEKEAEFEALAIMANASODALPIYQLOVENGED 1215
 DB 946 LSPKAEKNDTYKDDVHNOKCKEKEAEFEALAIMANASODALPIYQLOVENGED 1005
 QY 1216 IITIQDPTPEPLPGHTAKOPYREDTEMLNGOQIGLAFSSCYAOQVGTTLMAVQVY 1275
 DB 1006 IITIQDPTPEPLPGHTAKOPYREDTEMLNGOQIGLAFSSCYAOQVGTTLMAVQVY 1065
 QY 1276 YVRNTSSEOEVEVVALREERIRMSHLNHPNIRIMGATCEKSNLFIEMWAGSVAHLL 1335
 DB 1066 YVRNTSSEOEVEVVALREERIRMSHLNHPNIRIMGATCEKSNLFIEMWAGSVAHLL 1125
 QY 1336 SKYAFKESVYINTEDQLRGLSTLHENQIIRHVKGANLLIDSTGRLRIADFGAARL 1395
 DB 1126 SKYAFKESVYINTEDQLRGLSTLHENQIIRHVKGANLLIDSTGRLRIADFGAARL 1185
 QY 1396 ASKGTGAGEPQGLGTLAFAPVYLVNGOQYGRSCDVWVSCATTEWAKAPPMANAKHS 1455
 DB 1186 ASKGTGAGEPQGLGTLAFAPVYLVNGOQYGRSCDVWVSCATTEWAKAPPMANAKHS 1245
 QY 1456 NHALIFKIASATTAPSIPIHLSGLRDVALRCLDELOPDRPSPRELLKHPVFRTW 1512
 DB 1246 NHALIFKIASATTAPSIPIHLSGLRDVALRCLDELOPDRPSPRELLKHPVFRTW 1302
 RESULT 10
 AAR66029
 ID AAR66029 standard; Protein: 672 AA.
 XX
 AC AAR66029;
 DT 28-JUN-1995 (first entry)
 XX
 DE Mammalian MEK kinase (MEK1).
 XX
 KW MEK kinase; MEK1; mitogen-activated protein kinase regulator;
 KW MAPK; cell atrophy inhibition; Parkinson's; Alzheimer's; cancer;
 KW autoimmune diseases; allergies; wound healing; oncogenes;
 KW tumour agents; neurotropic growth factor.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..210
 FT /note="amino terminus regulatory domain"
 FT Region 211..215
 FT /note="regulatory hinge sequence"
 FT Domain 401..672
 FT /note="catalytic domain"
 PN WO9424159-A.
 PD 27-OCT-1994.
 XX
 PF 15-APR-1994; 94WO-US04178.
 XX
 PR 15-APR-1993; 93US-0049254.
 XX
 PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX
 PI Johnson GL;
 XX

DR MPI: 1994-357747/44.
 N-PSDB: AAQ79325.
 XX New MEK kinase protein and related antibodies and nucleic acid
 PT regulator of mitogen activated protein kinase, useful
 PT therapeutically to inhibit cell atrophy, to screen for oncogenes
 PT etc.
 XX
 XX Claim 6: Page 8: 84pp: English.
 XX
 CC AAQ79325 encodes AAR66029 the mammalian MEK kinase (MEK1), other
 CC unique mammalian MEK kinases identified by PCR are described in
 CC AAR66030 (MEK2), AAR66031 (MEK3) and AAR66032 (MEK4). MEK is an
 CC activator, independent of Raf protein, of mitogen-activated protein
 CC kinases (MAPK). Inactivation of MEK can be used in the treatment
 CC of some cancers, autoimmune diseases and allergies, while
 CC stimulation can promote wound healing. MEK can also be used to
 CC alleviate cellular atrophy in Parkinson's or Alzheimer's by acting
 CC as a neurotrophic growth factor, and to screen for oncogenes and
 CC tumour agents.
 CC
 XX
 XX Sequence 672 AA:
 SQ
 Query Match 39.6%; Score 3102.5; DB 15; Length 672;
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;
 Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

DB 646 VRCLEIOPDRPPRELLKHPVFRITW 672
 RESULT 11
 AAM56157
 ID AAM56157 standard; Protein; 672 AA.
 XX
 XX AAM56157;
 AC
 XX
 XX 17-JUL-1998 (first entry)
 DT
 XX
 DE A murine mitogen-activated protein kinase kinase (MAPKK).
 XX
 KW Mitogen-activated protein kinase kinase; MAPKK; mouse;
 KW extracellular signal-regulated kinase kinase; MEKK; regulation;
 KW signal transduction; raf-independent arm; screening assay; treatment;
 KW disorder; cancer; autoimmune disease; inflammation; allergy;
 KW neuronal disease; Parkinson's disease; Alzheimer's disease; ds.
 XX
 XX Mus sp.
 OS
 XX
 XX US5753446-A.
 PN
 XX
 PD 19-MAY-1998.
 XX
 PF 06-JUN-1995; 95US-0472934.
 XX
 PR 15-APR-1993; 93US-0049254.
 PR 14-OCT-1994; 94US-0323460.
 PR 21-FEB-1995; 95US-0354516.
 PR 12-MAY-1995; 95US-0440421.
 XX
 PA (NAE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 PI
 XX
 PI Johnson GL;
 XX
 DR MPI: 1998-311395/27.
 DR N-PSDB: AAY22676.
 XX
 XX Screening assay for regulators of MEK signal transduction - using
 PT mammalian MEK polypeptide
 PT
 XX
 PS Claim 13; Columns 33-38; 48pp; English.
 XX
 CC The present sequence represents a murine mitogen-activated protein kinase
 CC kinase (MAPKK) (also known as extracellular signal-regulated kinase
 CC kinase (MEKK)). The protein, which is serine/threonine kinase is capable
 CC of regulating signal transduction in cells. It regulates the activity of
 CC elements of the raf-independent arm of MEK. A screening assay for
 CC compounds that regulate signal transduction by a MEK protein comprises
 CC contacting a reaction mixture containing a mammalian MEK polypeptide and
 CC a test compound and determining the effect of the test compound on an
 CC indicator of signal transduction by the MEK polypeptide in the reaction
 CC mixture. Compounds identified by the above assay can be used to prepare
 CC therapeutic compositions for treating disorders that are subject to
 CC regulation or cure by manipulating a signal transduction pathway in
 CC cells involved in the disorders, e.g. cancer, autoimmune diseases,
 CC inflammations, allergies, and neuronal diseases such as Parkinson's
 CC disease and Alzheimer's disease.
 CC
 XX
 XX Sequence 672 AA:
 SQ
 Query Match 39.6%; Score 3102.5; DB 19; Length 672;
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;
 Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

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QY 946 TTTTQPKPMVOTKGRPHSCLNSSLHSQMLFPAIISTPSSSTPVPACATADVSKHR 1005
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113 -TTTEQPKPAVOTKGRPHSCLNSSLHS -HAQLMFAPASAPCSSAPSV-----DISKHR 165
QY 1006 LQGFIPCRIPASPOQORFKFSLOFHRNCPENKSDKLSPVFTQSRPLPSSNIHRKPSRP 1065
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 PQAIVPCKIPASPOQORFKFSLOFHRNCPENKSDKLSPVFTQSRPPSSNIHRKPSRP 225
QY 1066 TPQNTSKQGPSPKSMITLDLNNSSKCDSDFCSSNSSNAVIPSDETVTPPEKCRIDVN 1125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 VPQSTSKLGGATKSSMTLDLGSASRCDDSFSGGSGNSGNAVIPSEYVFTPEKCRIDVN 285
QY 1126 TELNSSIEDLLEASMPSSDITVTFKSEYAVLSPKAEENDTYKDVNHNOKCKEKMEAE 1185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 286 TELNSSIEDLLEASMPSSDITVTFKSEYAVLSPKAEENDTYKDVNHNOKCKEKMEAE 345
QY 1186 EELALIAMAMASODALPIYPQLOVENGEDIIIIQODTPETLPCHTRAKQPYREDTEMK 1245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 EELALIAMAMASODALPIYPQLOVENGEDIIIIQODTPETLPCHTRAKQPYREDTEMK 405
QY 1246 GQOIGLGFSSCYQAQDVGTGTLMAVKQVTVYRNTSSQEEVVALREETIMMSHLHPN 1305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 406 GQOIGLGFSSCYQAQDVGTGTLMAVKQVTVYRNTSSQEEVVALREETIMMCHLHPN 465
QY 1306 IIRMLGATCEKSNYNLFIEWAGGSVAHLISKYAFKESVYINTTEOLLRGLSTLHENQI 1365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 466 IIRMLGATCEKSNYNLFIEWAGGSVAHLISKYAFKESVYINTTEOLLRGLSTLHENQI 525
QY 1366 IHRDVKGANLLIDSTGRLRIADFGAARLASKGTGAFEGGOLLGTLAFAPREVLRGQO 1425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 526 IHRDVKGANLLIDSTGRLRIADFGAARLASKGTGAFEGGOLLGTLAFAPREVLRGQO 585
QY 1426 YGRSCDVWSVGCALIEEMACAPPMNAEKHSNHLALIFKIASATTAPSIPLSLGLRDVA 1485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 586 YGRSCDVWSVGCALIEEMACAPPMNAEKHSNHLALIFKIASATTAPSIPLSLGLRDVA 645
QY 1486 LRCLLELOPQDRPPSRELLKHPVFRTTW 1512
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 VRCLLELOPQDRPPSRELLKHPVFRTTW 672
RESULT 12
AA143318
ID AAY43318 standard; Protein; 672 AA.
XX
XX AAY43318;
XX
XX 24-JAN-2000 (first entry)
XX
XX Mitogen ERK kinase kinase, MEKK-1, protein sequence.
XX
XX Mitogen ERK kinase kinase; MEKK; MEKK-1; neurological disorder; cancer;
KM extracellular signal-regulated kinase; inflammation; autoimmune disease;
XX allergic reaction; hormone related disease; therapy.
XX
XX Mus sp.
XX
XX US5981265-A.
XX
XX 09-NOV-1999.
XX
XX 05-JUN-1995; 9505-0461146.
XX
XX 15-APR-1993; 9305-0049254.
XX
XX 12-MAY-1995; 9505-0440421.
XX
XX 15-APR-1994; 94WO-0504178.
XX
XX 14-OCT-1994; 94US-0323460.
XX
XX 14-OCT-1994; 94WO-US11690.
XX
XX 28-NOV-1994; 94US-0345516.
XX
XX
XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
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PI Johnson GL;
XX
XX WPI: 1999-633328/54.
DR N-PDB; AA231877.
XX
PT Regulating mitogen extracellular signal-regulated kinase protein
PT activity, useful for the treatment of cancer, neurological diseases and
PT autoimmune diseases
XX
PS Claim 2; Column 49-54; 94pp; English.
XX
CC This sequence is the mitogen ERK (extracellular signal-regulated
CC kinase) kinase kinase-1 (MEKK-1). The invention relates to a method of
CC regulating MEKK protein activity in a fungal cell by transforming or
CC transfecting the cell with a nucleic acid encoding an MEKK protein. The
CC MEKK protein is useful for treating cancer, inflammation, neurological
CC disorders, autoimmune diseases, allergic reactions, and hormone related
CC diseases.
XX
SQ Sequence 672 AA;
XX
Query Match 39.6%; Score 3102.5; DB 20; Length 672;
Best Local Similarity 89.2%; Pred. No. 1.8e-206;
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;
QY 826 MVTTPVHFYSKILMLSVSSSTHFTRRRRRLMAIADEVEIAEAIQAGVEDTLGQODSFL 885
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MVTAVPAVFSKLVYMLNAGSTHFTRRRRRLMAIADEVEIAEAIQAGVEDTVGDHDS-L 59
QY 886 QASVPNNYLETTESSPECTVHLEKTKGICATLKSASSEDISRLASISVGPSSSTTTT 945
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 QAVAPITCL--ENSSLEHTVHRKRTGKGLSATRLSASSEDISRLAGVSGVLPSS---- 112
QY 946 TTTTQPKPMVOTKGRPHSCLNSSLHSQMLFPAIISTPSSSTPVPACATADVSKHR 1005
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113 -TTTEQPKPAVOTKGRPHSCLNSSLHS -HAQLMFAPASAPCSSAPSV-----DISKHR 165
QY 1006 LQGFIPCRIPASPOQORFKFSLOFHRNCPENKSDKLSPVFTQSRPLPSSNIHRKPSRP 1065
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 PQAIVPCKIPASPOQORFKFSLOFHRNCPENKSDKLSPVFTQSRPPSSNIHRKPSRP 225
QY 1066 TPQNTSKQGPSPKSMITLDLNNSSKCDSDFCSSNSSNAVIPSDETVTPPEKCRIDVN 1125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 VPQSTSKLGGATKSSMTLDLGSASRCDDSFSGGSGNSGNAVIPSEYVFTPEKCRIDVN 285
QY 1246 GQOIGLGFSSCYQAQDVGTGTLMAVKQVTVYRNTSSQEEVVALREETIMMSHLHPN 1305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 406 GQOIGLGFSSCYQAQDVGTGTLMAVKQVTVYRNTSSQEEVVALREETIMMCHLHPN 465
QY 1306 IIRMLGATCEKSNYNLFIEWAGGSVAHLISKYAFKESVYINTTEOLLRGLSTLHENQI 1365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 466 IIRMLGATCEKSNYNLFIEWAGGSVAHLISKYAFKESVYINTTEOLLRGLSTLHENQI 525
QY 1366 IHRDVKGANLLIDSTGRLRIADFGAARLASKGTGAFEGGOLLGTLAFAPREVLRGQO 1425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 526 IHRDVKGANLLIDSTGRLRIADFGAARLASKGTGAFEGGOLLGTLAFAPREVLRGQO 585
QY 1426 YGRSCDVWSVGCALIEEMACAPPMNAEKHSNHLALIFKIASATTAPSIPLSLGLRDVA 1485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 586 YGRSCDVWSVGCALIEEMACAPPMNAEKHSNHLALIFKIASATTAPSIPLSLGLRDVA 645
QY 1486 LRCLLELOPQDRPPSRELLKHPVFRTTW 1512
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 VRCLLELOPQDRPPSRELLKHPVFRTTW 672
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PR 21-FEB-1995; 9505-0354516.
 XX (NAUJ-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 PA Johnson GL;
 XX WPI: 2000-411281/35.
 XX N-PSDB: AAA49222.
 DR
 XX Novel mitogen extracellular signal-regulated kinase kinase (MEKK)
 PT protein useful for treating cancer, inflammation, autoimmune diseases,
 PT neurological disorders and hormone related disease in animals
 XX
 PS Disclosure; Column 54-56; 92pp; English.
 XX
 CC The present sequence is the murine mitogen ERK kinase kinase (MEKK1)
 CC protein sequence. MEKK1 is involved in a signal transduction pathway
 CC which can ultimately lead to apoptosis. The proteins regulated by MEKK1
 CC include the MEK and MAPK proteins and c-Myc. Its coding sequence was
 CC identified by searching a mouse liver cDNA library for sequences similar
 CC to the Ste11 and Byr2 genes from yeast (these are MEKK homologues). The
 CC gene and protein can be used to treat diseases such as cancer,
 CC autoimmune disease, inflammatory responses, allergic responses and
 CC neuronal disorders including Parkinson's disease and Alzheimer's disease.
 XX
 SQ Sequence 672 AA:
 Query Match 39.6%; Score 3102.5; DB 21; Length 672;
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;
 Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;
 QY 826 MTTTVPVHVFPSKLLMLSVSSSTHTFTMRRLMAIDVEVIAEVLQIGVEDTLDGQDSFL 885
 DB 1 MTTAVPAVPSKLTVMASGTHFTMRRLMAIDVEVIAEVLQIGVEDTLDGQDSFL 59
 QY 886 QASVPNNYLETNTSSPECTVHLEKTKGICATKLSASSDISERLASISVGSSTTTT 945
 DB 60 QAAVAPISCL---ENSSLEHTVHREKTKGKLSATRLSSASSDISDRLAGVSVGLPSS--- 112
 QY 946 TTTTEQPKPMVOTKGRPHSQCINSSPLSHSOLMFPALSTPSSSTPSVPAGTATDVSKHR 1005
 DB 113 -TTTEQPKPMVOTKGRPHSQCINSSPLSHSOLMFPALSTPSSSTPSVPAGTATDVSKHR 165
 QY 1006 LQGFICRIPASPTQTKRSLQPHNCPENKSDKISLPFTOSRPLPSSNIHPRKPSRP 1065
 DB 166 PQAFVPECKIPASPTQTKRSLQPHNCPENKSDKISLPFTOSRPLPSSNIHPRKPSRP 225
 QY 1066 TPQNTSKQGPSPKNSMTLDLNNSSKCDSDSFGCSNNSNAVIPSDENYFTPEVEKCRDYN 1125
 DB 226 VPESTKLGDAITKSMTLDGASRCDDSGGSGNNAVIPSDEYVFTPEVEKCRDYN 285
 QY 1126 TELNSSIEDLLLEASMPSSDITVTFKSEAVLSPEKAENDDTYKDDVHNOKCKEKEMAEE 1185
 DB 286 TELNSSIEDLLLEASMPSSDITVTFKSEAVLSPEKAENDDTYKDDVHNOKCKEKEMAEE 345
 QY 1186 EELALATAMMASQDALPIYPOLOVENGEDIIIIODPTETLPGHTRKAKQPYREDLWMLK 1245
 DB 346 EELALATAMMASQDALPIYPOLOVENGEDIIIIODPTETLPGHTRKAKQPYREDLWMLK 405
 QY 1246 GQOIGLGAFFSCTQADVDVGTGLMAVKQVTVYNTSSSEQEVVEALREETRMASHNHPN 1305
 DB 406 GQOIGLGAFFSCTQADVDVGTGLMAVKQVTVYNTSSSEQEVVEALREETRMASHNHPN 465
 QY 1306 IIRMLGATCEKSNYNLEIEMMAGSVAAHLISKYGAFKESVIVYNTQDLGLGLYLEHNOI 1365
 DB 466 IIRMLGATCEKSNYNLEIEMMAGSVAAHLISKYGAFKESVIVYNTQDLGLGLYLEHNOI 525
 QY 1366 IIRHDVVGANLLIDSTGQRRIADFGAARLASGTGAGEGQGLGTIAVMADEVLRGQO 1425
 DB 526 IIRHDVVGANLLIDSTGQRRIADFGAARLASGTGAGEGQGLGTIAVMADEVLRGQO 585
 QY 1426 YGRSCDWMSVGCALIEEMACAKPPMNAEKHSNHLALIFKIASATTAIPSHLSPGLRDVA 1485
 |||||||

DB 586 YGRSCDWMSVGCALIEEMACAKPPMNAEKHSNHLALIFKIASATTAIPSHLSPGLRDVA 645
 QY 1486 LRCLLELOPODRPPSRRLKHPVFTTW 1512
 DB 646 VRCLLELOPODRPPSRRLKHPVFTTW 672
 RESULT 15
 ID AAA48934
 ID AAA48934 standard; Protein; 672 AA.
 AC AAA48934;
 XX
 XX 19-APR-2002 (first entry)
 DE Murine MEKK1-1.
 XX
 KW Mouse; MEKK1; mitogen ERK kinase kinase; enzyme; cancer; neuroprotective;
 KW autoimmune disease; signal transduction; allergy; inflammation;
 KW neurological disorder; hormone-related disease; apoptosis; infection;
 KW cytosolic; immunosuppressive; antiinflammatory; antiallergic;
 KW neurotropic; antiparkinsonian; contraceptive.
 XX
 OS Mus musculus.
 XX
 PN US633170-B1.
 XX
 PD 25-DEC-2001.
 XX
 PF 05-APR-1996; 9605-0628829.
 XX
 PR 15-APR-1993; 9305-0049254.
 PR 14-OCT-1994; 9405-0323460.
 PR 12-MAY-1995; 9505-0440421.
 PR 06-JUN-1995; 9505-0472934.
 XX
 PA (NAUJ-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX
 PI Johnson GL;
 XX
 DR WPI: 2000-163179/21.
 DR N-PSDB: AAL41577.
 XX
 PT New isolated nucleic acid encoding mitogen extracellular
 PT signal-regulated kinase kinase, useful for gene therapy of e.g. cancer
 PT and for recombinant protein production
 XX
 PS Claim 3; Column 107-110; 125pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of murine mitogen extracellular signal-regulated kinase (ERK)
 CC kinase kinase (MEKK) enzymes. The sequences can be used to treat a wide
 CC range of diseases including cancer, autoimmune diseases, inflammation,
 CC allergies, degenerative neurological diseases and hormone-related
 CC diseases, and for inhibiting spermatogenesis or oocyte maturation for
 CC contraception. The present sequence is the murine MEKK1.1 protein
 CC sequence.
 XX
 SQ Sequence 672 AA:
 Query Match 39.6%; Score 3102.5; DB 23; Length 672;
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;
 Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;
 QY 826 MTTTVPVHVFPSKLLMLSVSSSTHTFTMRRLMAIDVEVIAEVLQIGVEDTLDGQDSFL 885
 DB 1 MTTAVPAVPSKLTVMASGTHFTMRRLMAIDVEVIAEVLQIGVEDTLDGQDSFL 59
 QY 886 QASVPNNYLETNTSSPECTVHLEKTKGICATKLSASSDISERLASISVGSSTTTT 945
 DB 60 QAAVAPISCL---ENSSLEHTVHREKTKGKLSATRLSSASSDISDRLAGVSVGLPSS--- 112
 QY 946 TTTTEQPKPMVOTKGRPHSQCINSSPLSHSOLMFPALSTPSSSTPSVPAGTATDVSKHR 1005
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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 113 -TTTQPKPAVOTKGRPHSOCLNNSPLS-HAQLMFPAPAPCCSAPSP-----DISKRR 165

OY 1006 LOGFIPCRIIPASPOQRKFSLOFHRNCPENKDSKLSPTQSRPLPSSNIHRPKPSRP 1065
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 166 PQAFVPCRIIPASPOQRKFSLOFHRNCPENKDSKLSPTQSRPLPSSNIHRPKPSRP 225

OY 1066 TPGNTSKQDPSKNSMTLNLSSSKCDSFGCCSSNSNAVIPSDETFTVPVECKRDLVN 1125
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 226 YGISTSKLDGDKSSMTLDLGSASRCDSDFFGGGNSGNAVIPSDETFTVPVECKRDLVN 285

OY 1126 TELNSSIEDLLEASMPSSDTWTYFKSEVAVLSPEKAENDDTYKDDVNHNOCKEKEARE 1185
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 286 TELNSSIEDLLEASMPSSDTWTYFKSEVAVLSPEKAENDDTYKDDVNHNOCKEKEARE 345

OY 1186 EEALAIAMMASODALPIVPOLOVENGEDIIIOODTPETLPGHTKAKOPYREDTEWLK 1245
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 346 EEALAIAMMASODALPIVPOLOVENGEDIIIOODTPETLPGHTKAKOPYREDTEWLK 405

OY 1246 GQOIGLGAFFSCYQADVGTGTLMAVKOVTYVRNTSSQOEVEVEALREIRMMSHLNHPN 1305
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 406 GQOIGLGAFFSCYQADVGTGTLMAVKOVTYVRNTSSQOEVEVEALREIRMMSHLNHPN 465

OY 1306 IIRMLGATCEKSNYNLFITMMAGGSVAHLISKYAFKESVINYTEQLRGSLYLHENOI 1365
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 466 IIRMLGATCEKSNYNLFITMMAGGSVAHLISKYAFKESVINYTEQLRGSLYLHENOI 525

OY 1366 IHRDYKGANLLIDSTGOURLRIADFGAARLASKTGAGEFOGQLGTTAFMAPEVLRGOO 1425
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 526 IHRDYKGANLLIDSTGOURLRIADFGAARLASKTGAGEFOGQLGTTAFMAPEVLRGOO 585

OY 1426 YGRSCDVMVSGCAIITEMCAKPPNAEKSHNLALIFKIASATITAPISPSHLSPLGRDVA 1485
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 586 YGRSCDVMVSGCAIITEMCAKPPNAEKSHNLALIFKIASATITAPISPSHLSPLGRDVA 645

OY 1486 LRCLLEQPODRPPSRRLKHPYFRFTTW 1512
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 646 VRCLLEQPODRPPSRRLKHPYFRFTTW 672

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Search completed: December 20, 2002, 16:22:19
 Job time : 66 secs

QY 425 CGCGCAGCCCGGGGAGAAAGCGGGCCCGCGCGCGCGCTCTCGACGCGGCCCGG 484
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 Db 362 CGCGCGAGCCCGGGGAGAGCGGGCCCGCGCGCGCGCTCTCGACGCGGCCCGG 421
 QY 485 CGGGGTGAGATGAGAAATTAAGAAATCTCAAAAGGGTTCGCAAGATGAGATGCTG 544
 |||||
 Db 422 CGGGTCTGAGATGAGAAATTAAGAAATCTCAAAAGGGTTCGCAAGATGAGATGCTG 481
 QY 545 CAGAGAACGAATGATCAGAGGAGAAACTGAAAGCACTGTATGCCAGCTTGAAAGCAG 604
 |||||
 Db 482 CAGAGAACGAATGATCAGAGGAGAAACTGAAAGCACTGTATGCCAGCTTGAAAGCAG 541
 QY 605 AATGGTGGAAAGGAGAAATAGGCGAGGGCTGTGTGTATTAACCAATCCAGTTAAAG 664
 |||||
 Db 542 AATGGTGGAAAGGAGAAATAGGCGAGGGCTGTGTGTATTAACCAATCCAGTTAAAG 601
 QY 665 GAGATGATCTGAAATGAATCACTTATGACAGTGAATCTCAGAGAGAGGTCGAGGCAAGT 724
 |||||
 Db 602 GAGATGATCTGAAATGAATCACTTATGACAGTGAATCTCAGAGAGAGGTCGAGGCAAGT 661
 QY 725 CGGCTTCACAGCTTCGCAAAAGGCGCAGAGTCTCTCTGCGCAACTCCCATCAGTTC 784
 |||||
 Db 662 CGGCTTCACAGCTTCGCAAAAGGCGCAGAGTCTCTCTGCGCAACTCCCATCAGTTC 721
 QY 785 GCACAGTGAATTCAGAAATCTCCAGAGAGTAAAGGAGAAAGAGTTTCCCATGCTTTTC 844
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 Db 722 GCACAGTGAATTCAGAAATCTCCAGAGAGTAAAGGAGAAAGAGTTTCCCATGCTTTTC 781
 QY 845 AGAGTGGCAGAAATCACACACCCCGGAAAGCCCTTCACAGATGGCTTCCTCCATATA 904
 |||||
 Db 782 AGAGTGGCAGAAATCACACACCCCGGAAAGCCCTTCACAGATGGCTTCCTCCATATA 841
 QY 905 GCCCTGAGAGAAACAAACCCCGTGTAAACAAAGTATGCGGGCCAGCTGTACTCTG 964
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 Db 842 GCCCTGAGAGAAACAAACCCCGTGTAAACAAAGTATGCGGGCCAGCTGTACTCTG 901
 QY 965 AGCAGATAGGGCTTAATCTTTCTGTATTTGAGAGAGACGCCAGCAATTAATACCGG 1024
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 Db 902 AGCAGATAGGGCTTAATCTTTCTGTATTTGAGAGAGACGCCAGCAATTAATACCGG 961
 QY 1025 TGTATTATGGGCTCGAAGCTGAGCTGTGACGTGGAACATTCTGTATTCATCTGTA 1084
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 Db 962 TGTATTATGGGCTCGAAGCTGAGCTGTGACGTGGAACATTCTGTATTCATCTGTA 1021
 QY 1085 TTGTGATGCTCGGGGTGTTTCAACTAGAACTTCAGACCCCAATGTTATGAGAGAAACTT 1144
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 Db 1022 TTGTGATGCTCGGGGTGTTTCAACTAGAACTTCAGACCCCAATGTTATGAGAGAAACTT 1081
 QY 1145 TTAAGAAATTTAGAGTTGAGAGTTTGTTCAGAGAAATATCAGATAGGCTAGCTCAAG 1204
 |||||
 Db 1082 TTAAGAAATTTAGAGTTGAGAGTTTGTTCAGAGAAATATCAGATAGGCTAGCTCAAG 1141
 QY 1205 TCAAAAGCTCATCTGCTAATCAGACATCAGAAAGTTTGTTCAGAGATGCAAAATTCATA 1264
 |||||
 Db 1142 TCAAAAGCTCATCTGCTAATCAGACATCAGAAAGTTTGTTCAGAGATGCAAAATTCATA 1201
 QY 1265 CATGTGATCATCTAGTACTTCTAGCTTCTAGTTCAGAGAAACAGCATTAAGATGAAG 1324
 |||||
 Db 1202 CATGTGATCATCTAGTACTTCTAGCTTCTAGTTCAGAGAAACAGCATTAAGATGAAG 1261
 QY 1325 AACAGATGCTCTATTTCTGTTGGGCAATGCTTGATCAGAGAAAGTCTTACAGTGTG 1384
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 Db 1262 AACAGATGCTCTATTTCTGTTGGGCAATGCTTGATCAGAGAAAGTCTTACAGTGTG 1321
 QY 1385 AAGAGGCTGAGAGAAACAGTGCACACCATGCAATGTCATTTGGGAGAGAGATGA 1444
 |||||
 Db 1322 AAGAGGCTGAGAGAAACAGTGCACACCATGCAATGTCATTTGGGAGAGAGATGA 1381
 QY 1445 GAAGAATAGAGAACTTTAATATGTCCTTTGTAGATCTAAGTGAAGATCTCATGAT 1504
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 Db 1382 GAAGAATAGAGAACTTTAATATGTCCTTTGTAGATCTAAGTGAAGATCTCATGAT 1441

QY 1505 TCTACAGCCAGAGATGTCAGATCTGTGGATTCCTCTCTTCCTTCAGAGCTGCACAG 1564
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 Db 1442 TCTACAGCCAGAGATGTCAGATCTGTGGATTCCTCTCTTCCTTCAGAGCTGCACAG 1501
 QY 1565 AGCAAAACCGTACAGAGAGAGCCCTTGGTGTGATCAGAGAAATTAAGAGCAATTTTA 1624
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 Db 1502 AGCAAAACCGTACAGAGAGAGCCCTTGGTGTGATCAGAGAAATTAAGAGCAATTTTA 1561
 QY 1625 ACCTTACTCATTTATGAGAACTCAGCAAAATCCCTCTCTTACAAAGATTAAGTGAAC 1684
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 Db 1562 ACCTTACTCATTTATGAGAACTCAGCAAAATCCCTCTCTTACAAAGATTAAGTGAAC 1621
 QY 1685 GATTTAGAGTGTGGAATGGAATCTGTTGGCTCTTATTTTCTAGAACTGGAATGTA 1744
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 Db 1622 GATTTAGAGTGTGGAATGGAATCTGTTGGCTCTTATTTTCTAGAACTGGAATGTA 1681
 QY 1745 GAGAGATGGCCCTCAGAGCCCTTCCATGATGTCAGTGGGGCCCTGCTTGGCAAAAG 1804
 |||||
 Db 1682 GAGAGATGGCCCTCAGAGCCCTTCCATGATGTCAGTGGGGCCCTGCTTGGCAAAAG 1741
 QY 1805 GGGAGAGCACTGGAAATTTCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1864
 |||||
 Db 1742 GGGAGAGCACTGGAAATTTCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1801
 QY 1865 GTGGTCTTCCAGAGCAGTATCTCAGAGAGATGTTGGAGAGCAGTCTGAGGCTTCT 1924
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 Db 1802 GTGGTCTTCCAGAGCAGTATCTCAGAGAGATGTTGGAGAGCAGTCTGAGGCTTCT 1861
 QY 1925 CAATGTCGTGCTGACCCGCTGTACAAAGTGTGCTGCTTGTAAACCTTAGAG 1984
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 Db 1862 CAATGTCGTGCTGACCCGCTGTACAAAGTGTGCTGCTTGTAAACCTTAGAG 1921
 QY 1985 CCATGCTGTATATATCTCTTCCAGAGTATAGCGGAAAGAAATCAAACTTCAGAGACTTC 2044
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 Db 1922 CCATGCTGTATATATCTCTTCCAGAGTATAGCGGAAAGAAATCAAACTTCAGAGACTTC 1981
 QY 2045 TCCAGCAGATTTGAGACACCATCTAGTCAAAATGTGTCAGATGCGCAATAGCCGCAAGTC 2104
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 Db 1982 TCCAGCAGATTTGAGACACCATCTAGTCAAAATGTGTCAGATGCGCAATAGCCGCAAGTC 2041
 QY 2105 AGCTGTCCATATCAGACAGTGTGGAAGTGTGCAAGAGGAGAGAGTGGCGAGTTC 2164
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 Db 2042 AGCTGTCCATATCAGACAGTGTGGAAGTGTGCAAGAGGAGAGAGTGGCGAGTTC 2101
 QY 2165 GCAGAGAAATATCTAAAGAGTGTGATCCATGTTATGTTGGTGTATATGCTTAAAT 2224
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 Db 2102 GCAGAGAAATATCTAAAGAGTGTGATCCATGTTATGTTGGTGTATATGCTTAAAT 2161
 QY 2225 GTATTTCTGGAACCAAACTGAATCAACAAATTTGCGAAGAACTTCTGGCCGCTTGTTC 2284
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 Db 2162 GTATTTCTGGAACCAAACTGAATCAACAAATTTGCGAAGAACTTCTGGCCGCTTGTTC 2221
 QY 2285 TTATATATATGAGCTGTGTTGGAATTCCTGTGAATTTATCTCATATTTGTCAGATG 2344
 |||||
 Db 2222 TTATATATATGAGCTGTGTTGGAATTCCTGTGAATTTATCTCATATTTGTCAGATG 2281
 QY 2345 ATGTTTCAACAGCTGACCTGTTGGAATCAGATTAAGAAAGTGTGCTCTTAAACCT 2404
 |||||
 Db 2282 ATGTTTCAACAGCTGACCTGTTGGAATCAGATTAAGAAAGTGTGCTCTTAAACCT 2341
 QY 2405 TTGCTTTCAGATCATTGATTAATTCCTCAATCAATGTTGGCAAACTTCTCAGAGAGATCT 2464
 |||||
 Db 2342 TTGCTTTCAGATCATTGATTAATTCCTCAATCAATGTTGGCAAACTTCTCAGAGAGATCT 2401
 QY 2465 ACTTGAAGTCTGCAAGAAAGTGTACAGATGATCCCATGCTTGTTCAAAGCTGTGA 2524
 |||||
 Db 2402 ACTTGAAGTCTGCAAGAAAGTGTACAGATGATCCCATGCTTGTTCAAAGCTGTGA 2461
 QY 2525 TGTGAGTGTTCAGAG--TTCACATCAGCTTACAGAGATGAGTGGCCGCTTGTATGAGTA 2581
 |||||
 Db 2462 TGTGAGTGTTCAGAGTGTTCACATCAGCTTACAGAGATGAGTGGCCGCTTGTATGAGTA 2521
 QY 2582 TTGCAATAGAGTGAATTTGCCGAAAGCATCCAGTTGGGCGTGAAGAGACCTTTGGATG 2641

Db	2532	ATGCAGATGAGGTGGAAATATGCCGAAGCCATCCAGTTGGGGCTAGAAACACTTTACAA	2581
Qy	2642	GTCAACAGCAGAC - - TTCTGAGGCACTCTGTCCCAACACTTCTGGAAACACAGA	2699
Db	2582	GACAAACAACAACAGCTTTTGGAGGCATCTGTCCCAACAACATCTGGAAACACAGA	2641
Qy	2700	GAACAGTGTCCCC - TGAGTGCACAGTCCATTTAGAGAAAAGTGGAAAAGATTAATGTCTA	2758
Db	2642	GAACAGTGTCCCCCTTGAGTGCACAGCTCATTTTGAAGAAAAGTGGAAAAGATTAATGTCTA	2701
Qy	2759	CAAAATTTGAGTGCAGTGTTCAGAGGACATTTCTGAGACAGTGGCCACGACTTTCAGTAGAC	2818
Db	2702	CAAAATTTGAGTGCAGTGTTCAGAGGACATTTCTGAGACAGTGGCCACGACTTTCAGTAGAC	2761
Qy	2819	CTTCTACTTACACAAACAACAACAACAAGAGACACCAAGCAATGGTGTCAA	2878
Db	2762	CTTCTACTTACACACACACACACACACACACACACACACACACCAAGCAATGGTGTCAA	2821
Qy	2879	CAAAAGCAGACCCACACAGTCACTGTTTGAAGTCTCTCTCTTATCTCATCATTTCCCAAT	2938
Db	2822	CAAAAGCAGACCCACACAGTCACTGTTTGAAGTCTCTCTCTTATCTCATCATTTCCCAAT	2881
Qy	2939	TAAATGTTCCAGCCTGTCTCAACCCCTTCTTCTTCTTCAACCCATCTGTACCAGTGGCACTG	2998
Db	2882	TAAATGTTCCAGCCTGTCTCAACCCCTTCTTCTTCTTCAACCCATCTGTACCAGTGGCACTG	2941
Qy	2999	CAACAGATGTCTCTAAGCATAAGACTTCAGAGATTCATTTCCCTGCAGAAATACCTTGAT	3058
Db	2942	CAACAGATGTCTCTAAGCATAAGACTTCAGAGATTCATTTCCCTGCAGAAATACCTTGAT	3001
Qy	3059	CTCCTCAACACACACGCGAAGTTTCTCTCAATTCACAGAAATCTGCTCGAAAACAAAG	3118
Db	3002	CTCCTCAACACACACGCGAAGTTTCTCTCAATTCACAGAAATCTGCTCGAAAACAAAG	3061
Qy	3119	ACTCAGATTAACATTTTCCCCCGCTTTTACACAGCAAGACCTTGGCCCTCGAATAACATAC	3178
Db	3062	ACTCAGATTAACATTTTCCCCCGCTTTTACACAGCAAGACCTTGGCCCTCGAATAACATAC	3121
Qy	3179	ACAGGCCAAAAGCCATCTAGACTTACCCACAGGTAAATCAAGTAACAGGAGATCCCTCAA	3238
Db	3122	ACAGGCCAAAAGCCATCTAGACTTACCCACAGGTAAATCAAGTAACAGGAGATCCCTCAA	3181
Qy	3239	AAATATACATAGACACTTGATCTGAACAGATGTTCCAAATGATATACAGCTTTGGCTCTA	3288
Db	3182	AAATATACATAGACACTTGATCTGAACAGATGTTCCAAATGATATACAGCTTTGGCTCTA	3241
Qy	3299	GCACCAATAGTAGTAATGCTGTATACCCAGTGCAGACAGACTGTCCACCACAGTAGAGG	3358
Db	3242	GCACCAATAGTAGTAATGCTGTATACCCAGTGCAGACAGACTGTCCACCACAGTAGAGG	3301
Qy	3359	AGAAATGCAGATTAGTGTCAATACAGAGCTCACTCCAGATTAGAGACCTTCTTGAG	3418
Db	3302	AGAAATGCAGATTAGTGTCAATACAGAGCTCACTCCAGATTAGAGACCTTCTTGAG	3361
Qy	3419	CATCTATAGCCTTCAAGTATACACAGTAACCTTTTAAGCACAAGTGTGTGCTGCTGTCC	3478
Db	3362	CATCTATAGCCTTCAAGTATACACAGTAACCTTTTAAGCACAAGTGTGTGCTGCTGTCC	3421
Qy	3479	CTGAAAAGGCTGAAAATGATGATACCTACAAAGATGATGTGAATCATATCAAAAGTGCA	3538
Db	3422	CTGAAAAGGCTGAAAATGATGATACCTACAAAGATGATGTGAATCATATCAAAAGTGCA	3481
Qy	3539	AAGGAAGATGGAAGGTGAAGGAAGAAAGCTTTAGCAATGCCATGGCATGTACAGGT	3598
Db	3482	AAGGAAGATGGAAGGTGAAGGAAGAAAGCTTTAGCAATGCCATGGCATGTACAGGT	3541
Qy	3599	CTCAGATGTGCTCTCCCATAGTTCTCACTCAGCTCAGGTTGAATATGGAAGAATATATCA	3658
Db	3542	CTCAGATGTGCTCTCCCATAGTTCTCACTCAGCTCAGGTTGAATATGGAAGAATATATCA	3601
Qy	3659	TTATATCAACAGATACACACAGAGACTCTACACAGACATACCAAGCAAAAACACCGTATA	3718

Db	3602	TTATTCAACGAGATACACCCAGAGACTCTACAGAGACATACCAACAAACAAACCGCTATA	3661
QY	3719	GAGAAAGACACTGMAATGGCTTTAAAGGTCAACAGATAGCGCTTGGAGCACTTTCTTGTGT	3778
Db	3662	GAGAAAGACACTGMAATGGCTTTAAAGGTCAACAGATAGCGCTTGGAGCACTTTCTTGTGT	3721
QY	3779	ATCAGGCTCAAGATAGTGGGAACAGCACTTTAATGGCTTTAAAGGAGCACTTTATGCA	3838
Db	3722	ATCAGGCTCAAGATAGTGGGAACAGCACTTTAATGGCTTTAAAGGAGCACTTTATGCA	3781
QY	3839	GAAACACATCTTCTGAGCAAGAAAGATAGAGCACTAAGAGAGATTAAGATGA	3898
Db	3782	GAAACACATCTTCTGAGCAAGAAAGATAGAGCACTAAGAGAGATTAAGATGA	3841
QY	3899	TGAGCCATCTGAAATCANTCCAAACATCATTAAGATGTGGGAGCCACAGTGTGAAGACCA	3958
Db	3842	TGAGCCATCTGAAATCANTCCAAACATCATTAAGATGTGGGAGCCACAGTGTGAAGACCA	3901
QY	3959	ATTACAAATCTCTTCATTAAGATGGACAGGGGGAGATGGGTGCTCATTTGTGAGTAAT	4018
Db	3902	ATTACAAATCTCTTCATTAAGATGGACAGGGGGAGATGGGTGCTCATTTGTGAGTAAT	3961
QY	4019	ATGGAAGCTTCAAAGAAATCAGTAGTATTATTACTACACTGAACAGTTACTCGGTGCTTT	4078
Db	3962	ATGGAAGCTTCAAAGAAATCAGTAGTATTATTACTACACTGAACAGTTACTCGGTGCTTT	4021
QY	4079	CGTATCTCCATGAAACCAATATCATTCACAGATATCTCAAAGGTGCTCAATTTGCTAATG	4138
Db	4022	CGTATCTCCATGAAACCAATATCATTCACAGATATCTCAAAGGTGCTCAATTTGCTAATG	4081
QY	4139	ACAGCACTGGTCAAGACATAAGAAATTGCAGATTTTGGAGCTGCAGCCAGGTGGCATCA	4198
Db	4082	ACAGCACTGGTCAAGACATAAGAAATTGCAGATTTTGGAGCTGCAGCCAGGTGGCATCA	4141
QY	4199	AAGAACTGGTGGCGAGGAGATTTTCAGGAGCAATTACTGGGGCAATTCGATTATTAAGCA	4258
Db	4142	AAGAACTGGTGGCGAGGAGATTTTCAGGAGCAATTACTGGGGCAATTCGATTATTAAGCA	4201
QY	4259	CTGAGGACTAAGAGGTCAACAGATATGAAGAGAGCTGTATGTATGAGACTGTGGCTGTG	4318
Db	4202	CTGAGGACTAAGAGGTCAACAGATATGAAGAGAGCTGTATGTATGAGACTGTGGCTGTG	4261
QY	4319	CTATTATAGAAGAAATGGCTTTGGCAAAACCAACATGAGAAATCAGAAAAACACTCCATCATC	4378
Db	4262	CTATTATAGAAGAAATGGCTTTGGCAAAACCAACATGAGAAATCAGAAAAACACTCCATCATC	4321
QY	4379	TTGCTTTGATATTAAAGATGTAGTGCAACTACTCTCATCGATCCCTTACATTGT	4438
Db	4322	TTGCTTTGATATTAAAGATGTAGTGCAACTACTCTCATCGATCCCTTACATTGT	4381
QY	4439	CTCTGGTTTACGAGATGTGGCTCTTGCTGTTTAAAGCTCAACCTCAGACAGACCTC	4498
Db	4382	CTCTGGTTTACGAGATGTGGCTCTTGCTGTTTAAAGCTCAACCTCAGACAGACCTC	4441
QY	4499	CATCAAGAGAGCTCTGCAACATCCAGCTCTTGCTGCTCAATGTATAGCCAAATTATGAGA	4558
Db	4442	CATCAAGAGAGCTCTGCAACATCCAGCTCTTGCTGCTCAATGTATAGCCAAATTATGAGA	4501
QY	4559	TCAACTACAGTAGAAGACGAGTGTCAACAGAGAAAAAAACTGTGGGGAACCACTT	4618
Db	4502	TCAACTAC -GTAGAGAAACAGAGATGTCTCAACAGAGAAAAAAACTGTGGGGAACCACTT	4561
QY	4619	GATATTCTACTGGCATGATGCCACATGACATAGAGTATGAACAGAGCCATGTGGGAAACCTT	4678
Db	4561	GATATT -CTAGGGCCAGAGTGCACATGAAACGATTAAGAACAGGCCATGTGGGAAACCTT	4618
QY	4679	ACCTAAATATGTGCAATACAAATCATGATCTTAAGCTAAAGTCAGATGCAAAAGCCCA	4738
Db	4619	ACCTAAATATGTGCAATACAAATCATGATCTTAAGCTAAAGTCAGATGCAAAAGCCCA	4678
QY	4739	ACTAGTCAGAAACT 4753	
Db	4679	ACTAGTCAGAAACT 4693	

Db 1659 TACAAAGATTGGCCGACGATGATTCAGGTGTTGGAATGGAACGCTTGCTGCTTA 1718
QY 1723 TTTTCTAGAAACTGGAATGTGAGAGATGGCCCTCAGGCGCTCTTCCCATGTGTCAGT 1782
Db 1719 TTTCTAGAAACTGGAACGTAAGGAAATGCGCCCTTAGCGTCTTCCACGAGCTTAGT 1778
QY 1783 GGGGCGCTGCTGTGGCAATGGGGAGAGACATCTGGGAAATCTGGGGCAGCAGTGGAAAC 1842
Db 1779 GGGGCGCTGCTGTGGCAATGGGGAGAGACATCTGGGAAATCTGGGGCAGCAGTGGGGC 1838
QY 1843 AGCCGAGTGGGGGAGGACGACGAGGCTCTCCAGACGATATCTGAGAGATGTTG 1902
Db 1839 AGCTTAAAGCGGGAGGAGGCGGAGGCTCTCCAGGCGCATCTGAGGAGATGTTG 1898
QY 1903 GAGGATGCTGACGCTTCTGTCAATGTCTGTGTCGACCTGTCTCAAAAGTGTACGT 1962
Db 1899 GAGGCGGCTGTGAGTGTCTGTCAATGTCTGTGTCGACCTGTCTCAAAAGTGTACGT 1958
QY 1963 GCTGCTTTAAAAACATTGAGAGGCAATGCTGTATACACTCTTGCCACAGCTGGGAGAA 2022
Db 1959 GCTGCTTTAAAAACATTGAGAGGCAATGCTGTATACACTCTTGCCACAGCTGGGAGAA 2018
QY 2023 AGAATTAACCTTCAGAGACTCTTCAGACGCAAGTGTAGACACATCTTAAGTCAATGTGCA 2082
Db 2019 AGAATTAACCTTCAGAGACTCTTCAGACGCAAGTGTAGACACTCTTGTCAAGTGTGCA 2078
QY 2083 GATGCCAATAGCCGACACAGTCACTGCTCCATATCAACACTGTGTGGAAGTGTGCAAGGC 2142
Db 2079 GATGCCAATAGCCGACACAGTCACTGCTCCATATCTCAAGTGTGGAAGTGTGCAAGGC 2138
QY 2143 CAAGCAGAGAGATTTGGCAGTGTGGCAGAAATCTAAAGCTGGATTCATTTGATTTG 2202
Db 2139 CAAGCAGAGAGATTTGGCAGTGTGGCAGAAATCTAAAGCTGGATTCATTTGATTTG 2198
QY 2203 GGTGTGATATATGCTTAATTTGATTTGATTTGGAACCAATGTAATCAATGTGCA 2262
Db 2199 GGTGTGATATATGCTTAATTTGATTTGATTTGGAACCAATGTAATCAATGTGCA 2258
QY 2263 GAACCTCTTGGCGCCCTTGTCTTATAGATAGATGTTGTTGGAATTTCCGTGTAATTT 2322
Db 2259 GAACCTCTTGGCGCCCTTGTCTTATAGACAGTTGCTGTTGGAATTTCCGTGTAATTT 2318
QY 2323 TATCTCAATATGTCAGTACTGATGTTTCAACAGCTGAGCCTGTTGAATAGTATAG 2382
Db 2319 TATCTCAATATGTCAGTACTGATGTTTCAACAGCTGAGCCTGTTGAATAGTATAG 2378
QY 2383 AAGCTGTGTCCTTCACTTACCTTGTGTCAGTCAATGATATTTCCCATCAATGTT 2442
Db 2379 AAGCTGTGTCCTTCACTTACCTTGTGTCAGTCAATGATATTTCCCATCAATGTT 2438
QY 2443 GGCAGAACTTTCAGAGAGATCTACTGATGTTGCAAGAAATGTTTACTACAGTACCCAT 2502
Db 2439 GGCAGAGTCTCTGAGAGATATATGAGCTCTCCAGAGATGTTGACCGACGCTCCGCT 2488
QY 2503 GTGTTTTCAGAACTGTTAGAAATGCTGAGTGTTCAGTTCCACTCACTTCCAGAGATG 2552
Db 2499 GTGTTTTCAGAACTGTTAGAAATGCTGAGTGTTCAGTTCCACTCACTTCCAGAGATG 2558
QY 2563 CGTGGCGCTTGTGATGCTTATTTGAGATGAGTGGAAATTTGCGGAAGCATCAATGGGC 2622
Db 2559 CGCGGCGCTTGTGATGCTTATTTGAGATGAGTGGAAATTTGCGGAAGCATCAATGGGC 2618
QY 2623 GTAGAAAGCACTTGTGATGTTCAACAGAGACGCTTCTGCAAGCATGTTTCCCAAAAC 2682
Db 2619 GTGAGAGCACTGTTGATGTTGCAACAGAGACGCTTCTGCAAGCATGTTTCCCAAAAC 2675
QY 2683 TATCTGAAACACAGAGAAAGTTCCTGAGTGTGACAGTGTTCATTTAGAGAAACTGGA 2742
Db 2676 TGTCT-----AGAAACAGCTCCCTTGAAGACACAGTGTTCATTTAGAGAAACTGGA 2726
QY 2743 AAAGGATTTATGCTTACAAATTTAGTGGCAGTTTCAAGAGCATTTTCCAGAGAGCTGGCC 2802
Db 2727 AAAGGATTTATGCTTACAAATTTAGTGGCAGTGTTCAGAGAGCATTTTCTGAGAGACTGGCC 2786

QY 2803 AGCATTTCACTAGAGACCTTCTAGTTCACAAACAAACAAACACAGAGCAACCA 2862
Db 2787 GGCCTCTCTAGAGACTTCCAGCT-----CAACACAAACAGAAACCA 2831
QY 2863 AAGCAGTGGTTCAAAAG 2922
Db 2832 AAGCAG 2891
QY 2923 TCTCATATTTCCCAATTAATTTTCCAGAGCTTGTCAACAGAGAGAGAGAGAGAGAGAGAG 2982
Db 2892 TC---TCTAGTCAATTAATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2948
QY 2983 GTACAG 3042
Db 2949 GTCC-----CAGATATTTTCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2993
QY 3043 AGAATTAACCTTCTGATCTCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3102
Db 2994 AAGATTAACCTTCTGATCTCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3053
QY 3103 TGTCTGAG 3162
Db 3054 TGTCTGAG 3113
QY 3163 CCTTCAG 3222
Db 3114 CCTTCAG 3173
QY 3223 CAGGAGATCCCTCAAAAG 3282
Db 3174 CTAAGGAG 3233
QY 3283 GACAGCTTGTGCTAG 3342
Db 3234 GACAGCTTGTGCTAG 3293
QY 3343 TTCACCCAGTAG 3402
Db 3294 TTCACCCAGTAG 3353
QY 3403 GAGAGCTTCTTGAAGAGATCTATGCTTCAAGTATACAGAGAGAGAGAGAGAGAGAGAG 3462
Db 3354 GAGAGCTTCTTGAAGAGATCTATGCTTCAAGTATACAGAGAGAGAGAGAGAGAGAGAG 3413
QY 3463 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3522
Db 3414 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3473
QY 3523 CATATCAAAAGTCAAAAG 3582
Db 3474 CATATCAAAAGTCAAAAG 3533
QY 3583 ATGCAATGTGAGGCTGTCAGAGATGCTCCCATATGTTCTCTAGCTGAGAGAGAGAGAG 3642
Db 3534 ATGCAATGTGAGGCTGTCAGAGATGCTCCCATATGTTCTCTAGCTGAGAGAGAGAGAG 3593
QY 3643 GGAGAGATATCATATATATCAACAGAGATACACAGAGAGAGAGAGAGAGAGAGAGAGAG 3702
Db 3594 GGAGAGATATATCATATATCAACAGAGATACACAGAGAGAGAGAGAGAGAGAGAGAGAG 3653
QY 3703 GCAAAACAG 3762
Db 3654 GCGAAG 3713
QY 3763 GCATTTTCTTCTGTTATCTAGAGCTCAGAGATGTTGGAAGTGTGGAAGTGTGGAAGTGT 3822
Db 3714 GCATTTTCTTCTGTTATCTAGAGCTCAGAGATGTTGGAAGTGTGGAAGTGTGGAAGTGT 3773
QY 3823 CAGGTGATATGTCAG 3882
Db 3774 CAGGTGATATGTCAG 3833

QY	3883	GAAAGAGTAAAGATGATGAGCCATCTGAATTCATATCAAAACATCATTAAGATGTTGGAGCC	394.22
Db	3894	GAAAGATCCGGATGATGGGTACCTCCAAACATCCAAACATATCCGGATGCTGGGGCC	389.33
QY	3943	ACGTGTAGAAGACATTAACAATCTCTCATTTGAATGGATGGAGGGGATCGGTGGCT	400.20
Db	3894	ACGTGCAGAAAGAGACAATCTCAACCTCTTCATTTGATGGATGGCGGGAGATCTGTGGCT	395.33
QY	4003	CATTGGTGAATTAATATGAGAGCTTCAAGAAATACATGATTAATTAATACATGAAACAG	406.82
Db	3954	CACCTCTTGATGATTAATACGAGAGCTTTCAAAGAGTCAAGTGTATTAATTAATCACTGAGAG	401.33
QY	4063	TTACTCCGTGGCCCTTTCGTATTCATCTGAAGAAACAAATCATTCACAGAGATGTCAAAAGT	412.22
Db	4014	TTTACTGGGTGGCTTTCCTTCTATCTCCACAGAAACACAGATATTTACAGAGAGCTCAAAAGT	407.33
QY	4123	GCCAAATTTGCTAATTTGACAGCACTGGTCAAGACTTAAGAAATTCAGATTTTGGAGCTGCA	418.22
Db	4074	GCCAACTGCTCATTTGACAGCACCGGCTGAGAGCTGAGAAATTCAGACTTTTGGAGCTGCT	413.33
QY	4183	GCCAGGTTGGCATCAAAAAGAAATGGTGCAGAGAGATTTTCAGGGCAATTTACTGGGACAA	424.22
Db	4134	GCCAGGTTGGCATCAAAAAGAAACCGGTGAGAGAGATTCAGAGGCAATTTACTGGGACAA	419.33
QY	4243	ATTTCATTTTATGACACCTGAGACTTAAGAGGCAACAAGTATGAAAGAGGCGTGATGTA	430.22
Db	4194	ATTTCATTTTATGACAGCTGAGGCTGATGCTTAAGAGGCTACAGCAATATGTAAGAGCTGTGATGTA	425.33
QY	4303	TGAGATGTTGGCTGTGCTATTAATGAATGGCTGTGCAAAAACCAATGGAATGACAA	436.22
Db	4254	TGAGATGTTGGCTGTGCGCATTAATGAATAGGCTGTGCAAAAACCACTTGGAAATGACAA	431.33
QY	4363	AAACACTCCAAATATCTGCTTTGATATTTAAGATTTGCTAGTGCACATTAATGCTCATCG	442.22
Db	4314	AAACACTCCAAATATCTGCTGCTGATTAATGAATTTGCTAGGCAACATGCAACCGGCC	437.33
QY	4423	ATCCCTTACCATTTGCTCTCCTGGTTTACAGAGATGGGCTCTCGTTGTTTGAACCTTCAA	448.22
Db	4374	ATCCCTGACACCTGTGCTCCCGGGTCTGCGCGACATGGGCGTGGCTGCTTGAACCTTCAAG	443.33
QY	4483	CCTCAGACAGACCTCCATCAACAGAGACTGTAAGACATCCAGTCTTCTGTAACATATG	454.22
Db	4434	CCTCAGACACCGGCTCCGTTCCAGAGAGCTGTGAAGAAACATCCGGTCTTCCGTACACAGTGG	449.33
QY	4543	TAGCATTAATTTGAGATTCACATTAACATTAACAGAGATGCTTAACAAAGAAAAAACT	460.22
Db	4494	TAGCATTAATTTGAGATTCACATTAATGAAGACAGAGATTAATGCAACCGGAGAGAAAAAG	455.33
QY	4603	TG-----TGSGGAACCAATTTGATATTTCTAGTGGCCATGATGGCCATGGAACAGCTATGAC	465.88
Db	4554	AGAACTTGTGTGGGACCAATATGCGCTTAACCGCAGGCCCTCAGCGCACTGAACACCGAGAAC	461.33
QY	4659	GAGGCCAGTGGGAGAACCTTACCTAAGTATGATTTGACAAATCATCATGATCTGTACTAAG	471.88
Db	4614	GGGGCGACGGGGAA--CCGAACTTAAGCATGTGATTTGAACAAATCATGACGTGTACTAAG	467.22
QY	4719	CTCAGTATGCA--AAAGCCAAACTAGTGCAGAACTGTAACTGTGCTTCAAGAACT	477.77
Db	4673	CTCGATATGAGACATCTACAGCTGTGTGAGAACTGTGACACACCGTCTTTCACAGGACT	473.22
QY	4778	GAGCCATAGTGAACAGAAACAAATTAATTTGATGATGATGAAATTCAGAGAGCATTAATTT	483.77
Db	4733	GAGCTGTGGGGACCAAGAAAGCGCATGATGATTTGCAATTAAGAAAGAAAGCATTAATTT	479.22
QY	4838	TATTTTATTTTGGACACTTTTTCAGCAA 4864	
Db	4793	TA--TTTTTGAGACACTTTTTCAGCTA 4817	

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? GENERAL INFORMATION:
? APPLICANT: Johnson, Gary L.
? TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To Extracellular Matrix
? FILE REFERENCE: CFI-004DPCP3
? CURRENT APPLICATION NUMBER: US/08/628,829A
? CURRENT FILING DATE: 1996-04-05
? EARLIER APPLICATION NUMBER: 08/440,421
? EARLIER FILING DATE: 1995-05-15
? EARLIER APPLICATION NUMBER: 08/323,460
? EARLIER FILING DATE: 1994-10-14
? EARLIER APPLICATION NUMBER: 08/049,254
? EARLIER FILING DATE: 1993-05-15
? EARLIER APPLICATION NUMBER: 08/410,602
? EARLIER FILING DATE: 1995-04-24
? EARLIER APPLICATION NUMBER: 08/472,934
? EARLIER FILING DATE: 1995-06-06
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: SeqIdn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 5539
? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(4779)
? OS-08-628-829-3

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Query Match	64.6%;	Score 3387.6;	DB 4;	Length 5539;
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Matches 4075; Conservative 0; Mismatches 709; Indels 102; Gaps 16;

1 GAGAAATGCGCGCGCGCGGGAATCGCGCCTCGTCGTGGGATTCCCGGGCCAGG 60

Db 298 GAGAAATGGCGCGCGGGCGATCGCGCTCGTCTGGGATTCCCGGGCGCCGCG 35

61 GCTAGGAGCCCTGAGGCGCGGCGC-----GGAGGAGCCCTCAAGGCGAGCAGC 112

Db 358 GCGCGAGTCCCGAGCGCGCGCGCGAGGAGGAGGAGCTCTCCAGGGAACGCC 41

112 GCGCCCGCGGCTGCCGC - - GGACTGCTGCCGGAAGCGCGGCACGCGGGGCCCGCGGAGCGG 162

Db 418 GCGCCCGACGCGCGCGCGCGCTGCTGCGGGAGCCTGGCAGCGCGGGC-CGAGCGC 47

ov 169 GCGGACTTGGCGGCGGCGGCGGCGGCAAGCTTGGCGCAAAAGTGCGGGAAGTAGTGGAGCGTGGACACAGCGTCGCG 22

[illegible][illegible]

0b 537

[illegible]

A vertical ruler with markings from 0 to 10 cm. The markings are in millimeters, with numbers every centimeter. The ruler is oriented vertically with the 0 mark at the top.

A vertical ruler with markings from 0 to 10 cm. The markings are in millimeters, with major ticks every centimeter and minor ticks every millimeter. The ruler is oriented vertically with the 0 mark at the top.

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[illegible]

48 / C1C1GAGCGCCCGCGG1CG1GAGATGGAGAA1AAAGAAC1C1CAAGGG11GC 32

DD / 46 CCCTGCAAGCGCCCTCCGGTCGAGAGATGAAGAAACCTCAAGGACTC 80

521 ACAAGATGGATGATCGTCCAGAGGAACGAATGATCAGGGAGAACTGAAGGCAACCTGTA 58

Db 806 ACAGATGGAGGATCGCCCGGAGGAGAGAATGATCCGGGAGAGCTCAAGGCGACCTGTA 86

587 TGCAGCCTGGAAGCACGAATGCTTGGAAGGAGAATAGGCGAGGCCCTGTGGTGTA 64

Db 866 TGGCGGCTTGGAAGCAAGATGGTTGGAGAGAGAAAGAGAGAGGCGCTCTGTGTGTGA 925
QY 647 AACCAATCCCAATTAAAGAGATGATCTGAAATGAATCACTTAGCAGCTGAGCTTCAG 706
Db 926 AGCCAATCCCTATTAAAGAGATGATCTGAAATGAATCACTTAGCAGCTGAGGCGCCAG 985
QY 707 GAGAGTCCAGGCAATGGCGCTTCACAGCTTCGAAAGGCCAGAGAGCTTCCTCTG 766
Db 986 GAGAGGCGAGGAGGATCCCGTGCACAGCCCGCCAGAGGCGAGCGAAAGCCATCTCTG 1045
QY 767 GCAACTCCCATAGGATGGGACAGTGAATCAGAAATCTCCAGAGTAAAGAGAAAGAG 826
Db 1046 GCAGCTCTCCGTAGGCGCTCGGTGAAGCCGGAATCCAGAGATTAAGACGGAAAGAG 1105
QY 827 TTTCCCAAGTCCCTTTCAGAGTGGCAGAAATCACACACCCCGAGAGGCCCTTCACAG 886
Db 1106 TGTCCCGGCTTCAGAGTGGCAGAAATCACACACCCCGAGAGGCCCATACACGG 1165
QY 887 ATGGCTTTCACCATATAGCCCTGAGGAAACAAACCGCGCTTTAACAAATGTGCGGG 946
Db 1166 ATGGCTTTCACCGCTGACAGCCAGAGAGAGAGCGCGCGGTGAACAAAGTATGAGAG 1225
QY 947 CCAGACTGTAATCTACTGACAGCAGATAGGCGCTTAATCTTCGTGATGAGAGAGAGCC 1006
Db 1226 CCAGGCTGTAATCTGCTGACAGCAGATAGGAGCCCAACTCTTCGTGATGAGAGAGAG 1285
QY 1007 CAGACATAAATACCGGGTGTATTGGGCTCAGAACTGACAGCTGTGCACTGGAACAT 1066
Db 1286 CAGACATAAATACCGGGTGTATTGGGCTCAGAACTGACAGCTGTGAGGAGAGCAT 1345
QY 1067 TCTGTATTCATCTGCTATTTGTGATGCTCCGGGTGTTTCACTAGAACCTTCAGACCCA 1126
Db 1346 TCTGTATTCACCTCTGTTGTGATGCTCCGGGTGTTTCACTAGAACCTTCAGACCCA 1405
QY 1127 TGTATGAGAGAAATCTTAAAGATTTTGAAGTGGAGTTTGTTCAGAAATATACCA 1186
Db 1406 TGTATGAGAGAAATCTTAAAGATTTTGAAGTGGAGTTTGTTCAGAAATATACCA 1465
QY 1187 GTAAGGCTAGCTCAGAGATCAAAAGCTCATCTGTAAACACCATCAGAAATTTGTTTAC 1246
Db 1466 GTAAGGCTAGCTCAGAGATCAAAAGCTCATCTGTAAACACCATCAGAAATTTGTTTAC 1525
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Db 1526 GCATGTCAAAATTTCTCATCTTGTCTCATCTGTACTTCTAGCTCTAGTTAGAAAACA 1585
QY 1307 GCATTAAGATGAAGAGAGACAGATGTCTTAATTTGCTTGTGGGATCTGTATGAG 1366
Db 1586 GCATTAAGATGAAGAGAGACAGATGTCTTAATTTGCTTGTGGGATCTGTATGAG 1645
QY 1367 AAAGCTTACAGTGTGTGAAGAGGCTGAGAGAAAGAGTGCACACCACTGCATGTCA 1426
Db 1646 AAAGCTTACAGTGTGTGAAGAGGCTGAGAGAAAGAGTGCACACCACTGCATGTCA 1705
QY 1427 TTTGGGCAAGAAAGTGTGAAGAAATAGAAACCTTAAATATGTCCCTTTGTATGATCTA 1486
Db 1706 TCTGGGCGGAAAGTGTGAAGAAATAGAAACCTTAAATATGTCCCTTTGTATGATCTA 1765
QY 1487 AGTGAAGATCTCATGATTTTTCAGCCAGAGTGTGCAAGCTCTGTGATTTCCCTCTT 1546
Db 1766 AGTGAAGATCTCATGATTTTTCAGCCAGAGTGTGCAAGCTCTGTGATTTCCCTCTT 1825
QY 1547 CCCTCAGAGCTGCAGAGCAAAACCGTACAGAGAGCGCTTTGGCTGATCA---CGAA 1603
Db 1826 CCCTCAGAGCTGCAGAGCAAAACCGTACAGAGAGCGCTTTGGCTGATCA---CGAA 1885
QY 1604 GGAATCAAGAGAGCAATTTAACTTACTATTTATGAACTCAGCAAAATCCCTCTCTT 1663
Db 1886 GGAATCAAGAGAGCAATTTAACTTACTATTTATGAACTCAGCAAAATCCCTCTCTT 1945
QY 1664 ACAAAAGATTTAGCTGAGAGCATGATTCAGTGTGTAATGGAATGGAATGTTGGCTGAT 1723
Db 1946 ACAAAAGATTTAGCTGAGAGCATGATTCAGTGTGTAATGGAATGGAATGTTGGCTGAT 2005

QY 1724 TTTCTAGAACTGGAATGTGAGAGAGATGGCCCTCAGCGCTCTTTCCCATGATGTGATG 1783
Db 2006 TCTCTAGAACTGGAATGTGAGAGAGATGGCCCTCAGCGCTCTTTCCCATGATGTGATG 2065
QY 1784 GGGGCGCTGCTGTGGCAAAATGCGGAGAGCACTGGAATTTCTGGGGGAGAGAGTGAAGCA 1843
Db 2066 GGGGCGCTGCTGTGGCAAAATGCGGAGAGCACTGGAATTTCTGGGGGAGAGAGTGAAGCA 2125
QY 1844 GCCGAGTGGGGAGGAGCAGCAGTGGGTCTTCCAGACAGTATCTCAGAGATGTGGTGG 1903
Db 2126 GCTTAAGCGGGGAGGAGCGCCAGCGGGTCTTCCAGCCAGCATCTCAGGGGATGTGGTGG 2185
QY 1904 AGGCACTGTCAGCGCTTCTGTCAATGCTGTGTGACCTGTCTTACAAAGTATGCTTG 1963
Db 2186 AGGCACTGTCAGCGCTTCTGTCAATGCTGTGTGACCTGTCTTACAAAGTATGCTTG 2245
QY 1964 CTGCTTTAAATCAATTAAGAGCCATGCTGTGTATATCTCTTGGCAGAGTTAGCGGAA 2023
Db 2246 CTGCTTTAAATCAATTAAGAGCCATGCTGTGTATATCTCTTGGCAGAGTTAGCGGAA 2305
QY 2024 GAATCAAACTTCAGAGACTTCTCCAGCGAGTGTGAGACACCATCTGTGCAAAATGTGCA 2083
Db 2306 GAATCAAACTTCAGAGACTTCTCCAGCGAGTGTGAGACACCATCTGTGCAAAATGTGCA 2365
QY 2084 ATGCCAATAGCCGCAAGTCAAGCTGTCAATATCAACACTGTTGGAACTGTGCAAGGCC 2143
Db 2366 ATGCCAATAGCCGCAAGTCAAGCTGTCAATATCAACACTGTTGGAACTGTGCAAGGCC 2425
QY 2144 AAGCAGAGAGTGTGGCAGTTGGCAGAGAAATACTAAAAGCTGCATTTGATTTGGTG 2203
Db 2426 AAGCAGAGAGTGTGGCAGTTGGCAGAGAAATACTAAAAGCTGCATTTGATTTGGTG 2485
QY 2204 GTGTGATTAAGTCTTAATTTGATTTGTAAGAAACCAACTGAATCAAAATTTGGCAG 2263
Db 2486 GTGTGATTAAGTCTTAATTTGATTTGTAAGAAACCAACTGAATCAAAATTTGGCAG 2545
QY 2264 AACTCTTGGCGCGCTTGTCTTATAGATAGACTGTTGTAATTTCTGCTGAATTTT 2323
Db 2546 AACTCTTGGCGCGCTTGTCTTATAGATAGAGTTGCTGTGAAATTTCTGCTGAATTTT 2605
QY 2324 ATCTCATATTTGTCAGTACATGATGTTTTCACAGCTGAGCGCTTGTGAATATGATATAGA 2383
Db 2606 ATCTCATATTTGTCAGTACATGATGTTTTCACAGCTGAGCGCTTGTGAATATGATATAGA 2665
QY 2384 AGCTGCTGCTCCTTAACTTGTGCTTGTGCAAGTGCATTAATTTCCCACTCAATGCTTG 2443
Db 2666 AGCTGCTGCTCCTTAACTTGTGCTTGTGCAAGTGCATTAATTTCCCACTCAATGCTTG 2725
QY 2444 GCAAACTTTCAGAGAGATCTACTTGAATTCGCAAGATGTTACTACAGTACCCATG 2503
Db 2726 GCAAACTTTCAGAGAGATCTACTTGAATTCGCAAGATGTTACTACAGTACCCATG 2785
QY 2504 TGTTTTCAAAACCTTAAAGATGCTGAGTGTTCCTCAATTCACATCTTCAACAGATGCTG 2563
Db 2786 TGTTTTCAAAACCTTAAAGATGCTGAGTGTTCCTCAATTCACATCTTCAACAGATGCTG 2845
QY 2564 GTCGCGCTTGTGATGCTATTTGACATGAGTGAATTTGCCAGAGCCATCAGTGTGGCG 2623
Db 2846 GTCGCGCTTGTGATGCTATTTGACATGAGTGAATTTGCCAGAGCCATCAGTGTGGCG 2905
QY 2624 TAGAAGACCTTTGATGATGTCACAGAGACAGCTTCTTGCAGGCAATCTGTTCCCAACT 2683
Db 2906 TAGAAGACCTTTGATGATGTCACAGAGACAGCTTCTTGCAGGCAATCTGTTCCCAACT 2962
QY 2684 ATCTGGAAGACAGAGAAAGATTTCCCTGAGTGCACAGTCTATTTAGAGAAATCTGAA 2743
Db 2963 GTCT-----AGAAAGACAGTCCCTTGTGAGCACAGTCTATAGAGAAATCTGAA 3013
QY 2744 AAGGATTAATGCTACAAATTTGAGTGCAGTGTGAGAGGACATTTGAGAGAGCTGSCA 2803
Db 3014 AAGGATTAATGCTACAAATTTGAGTGCAGTGTGAGAGGACATTTGAGAGAGCTGSCC 3073

[illegible]

Db	4121	AAGAGATCCGGATGATGGGTACCTCAACATCCAAACATCATCCGAGATCGTGGGGCCCA	4180
Oy	3944	CGTGTGAAGAGCAATTACAAATCTCTTCATTGAATGATGGCAGGGGCATCGTGGCTC	4003
Db	4181	CGTGCAGAAAGAGCACTACAACTCTCTTCATTGATAGTGATGGCGGGAGGATCTGTGGCTC	4240
Oy	4004	ATTTCGAGAGTAAATATGAGACCTTCAAGAAATCACTACTATTTAACTCACTGAACGT	4063
Db	4241	ACCTCTTGAGTAAATACGGAGACTTTCAAGGAGTCACTGCTCATTAATCACTACCTGACACT	4300
Oy	4064	TACTCGGTGGCCTTTCGTATCTGCATGAAACCMAATCATTCACAGAGATGTCAAAAGGTG	4123
Db	4301	TACTGCGTGGCCTTTCCTATCTCCAGAGAACACAGATCATTCACAGAGACGTCAAAAGGTG	4360
Oy	4124	CCAAATTTGCTAAATTGACAGACATCGTGCAGAGACTAAGAAATTTGCACATTTTGGAGCTCGAG	4183
Db	4361	CCAACTGCTCATATTGACAGACCGGTGCAGAGGTGTGAATTTGCAGACTTTGGAAGCTGTGTG	4420
Oy	4184	CCAGGTGGGCACTCAAAAGAACTGGTGCAGAGAGATTTGAGGACAAATTACTGGGGACAA	4243
Db	4421	CCAGGTGGGCACTCAAAAGAAACCGGTGCAGAGAGATTTCCAGGGACAGATTACTGGGGACAA	4480
Oy	4244	TTGCATTATTAATGCACTGAGAGTCTAAGAGGTGCACAGTATGGAAGAGCTGTATAT	4303
Db	4481	TTTGATTTCAATGGCGCCCTGAGAGTCTCTAAGAGGTGCAGAGTATGGTGAAGCTGTATAT	4540
Oy	4304	GGAGTGTGGTGGCTGTGCAATTAATGAATAGGCTGTGCAAACACACATGGAAATGCGAGAA	4366
Db	4541	GGAGTGTGGTGGCTGGCATTTATGAATATGGCTGTGTGCAAACACACCTTGGAAATGCGAGAA	4600
Oy	4364	AACACTCCAAATCATCTTGGCTTTGATATTTAAGATTGCTAATGTCACACTACTGCTTCATGCA	4423
Db	4601	AACACTCCAAATCATCTGCTCTGATTAATTAAGATTGCTAAGCCAACTACTGCACGCTGCCA	4660
Oy	4424	TCCCTTCAACATTTGTGCTCCGAGTTTACAGAGATGGGCTTGTGGTTTGAACATCTCAAC	4483
Db	4661	TCCCGTACACACTGTCTCCCGGGGTCTGCGGACGTGGCGCTGCGCTGTTAAGAACTTCACG	4720
Oy	4484	CTCAGGACAGACCTCCATCAAGAGAGCTACGTGAAGCATCCACTCTTGTCTACTACATGGT	4543
Db	4721	CTCAGGACCGGCTCTCGGTCCAGAGAGCTGTGAACATCCGGTCTTCGTACACATGGT	4780
Oy	4544	AGCCAAATTAATGCAAGTAACTAAGATGAGAAACAGATGCTCAACAAGAGAAAAAACTT	4603
Db	4781	AGTTAAATTTGTCAGATCAGCTTAATGAGAACAGATGATGCAACCGGAGAGACGAAAGAA	4840
Oy	4604	G----TGGGAAACCACTTATATATTCTACAGGCAATGATGCACTGAACAGCTATGAGACG	4659
Db	4841	GAACTTTGTGGGCGACATGCGCGGTAAACCGAGGCCCTCAGCCATCGMAACGCGCAAAAGC	4900
Oy	4660	AGGCCAAGTGGGGAACCTTACCTAAGATGATGCAATTCATGATCTGTAACCTAAGC	4719
Db	4901	GGGCGCAACCGGGGAA--CCGTACTTAACCATGTGATTTACAAATCATAGACCTGTACTAAGC	4959
Oy	4720	TCATATATGCA--AAAGCCCAAACTAGTGCAGAAACGTAAACGTGCGCTTTCAAACAACGTG	4778
Db	4960	TCGATATATGCAACATCTACAGCTCTGTGCAGAGACTGCAACCGTGTCTTTCACAGACTG	5019
Oy	4779	GCCCTAGGTGAACGAAACCAATGAAAGTTTGCATGACTAAATTCAGAGAGCATTAATTT	4838
Db	5020	GCTGTGGGGACCCAGAAAGCGATGAGATTTGTCATGACTAAAGAACAGATTAATTT	5079
Oy	4839	ATTTTTGGAGCACTTTTTCACAA 4864	
Db	5080	A--TTTTTGGAGCACTTTTTCACCTA 5103	

RESULT 4
US-09-423-890-1
; Sequence 1, Application US/09423890
; Patent No. 6312934
; GENERAL INFORMATION:

APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEK1 PROTEIN AND NUCLEIC ACID MOLECULES
FILE REFERENCE: AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/423,890
CURRENT FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: USSN 60/078,153
PRIOR FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: USSN 60/099,165
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3911
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(3908)
US-09-423-890-1

Query Match 62.7%; Score 3286.4; DB 4; Length 3911;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

QY 590 CACCTTGAAGCAGATGTTGGAAGAGAAATAGGCGAGGCGCTGTGTGTAAC 649
DB 1 CGGCTGGGAAGCAGATGTTGGAAGAGAAATAGGCGAGGCGCTGTGTGTAAC 60
QY 650 CAATCCAGTTAAAGGAGATGATCTGAATGAATCATTAGACGATCTCCAGAG 709
DB 61 CAATCCAGTTAAAGGAGATGATCTGAATGAATCATTAGACGATCTCCAGAG 120
QY 710 AGGTCCAGGCAAGTGGCGCTTCCACAGCTTCCAAAGGCGAGCGAGTCTTCTGCA 769
DB 121 AGGTCCAGGCAAGTGGCGCTTCCACAGCTTCCAAAGGCGAGCGAGTCTTCTGCA 180
QY 770 ACTCCCATGAGTGGCGAGTGAATCAGATCTCCAGAGTGAAGAGAAAGATTT 829
DB 181 ACTCCCATGAGTGGCGAGTGAATCAGATCTCCAGAGTGAAGAGAAAGATTT 240
QY 830 CCCAGTGGCTTTTCAGAGTGGCAGAAATCAGACACCCGAGAGCCCTTCCAGAGT 889
DB 241 CCCAGTGGCTTTTCAGAGTGGCAGAAATCAGACACCCGAGAGCCCTTCCAGAGT 300
QY 890 GCTTCTCACCATTAGCCCTGAGGAAACAAACCGCGCTTTTAAACAAAGTATGCGGCA 949
DB 301 GCTTCTCACCATTAGCCCTGAGGAAACAAACCGCGCTTTTAAACAAAGTATGCGGCA 360
QY 950 GACTGATCTTACTGAGCAGATAGGCGCTTACTCTTCTGATTTGAGAGACAGCCAG 1009
DB 361 GACTGATCTTACTGAGCAGATAGGCGCTTACTCTTCTGATTTGAGAGACAGCCAG 420
QY 1010 ACAATAAATACCGGCTTATTTGGGCTCAGAACTGACACTGTCAGCGTGAACATTCT 1069
DB 421 ACAATAAATACCGGCTTATTTGGGCTCAGAACTGACACTGTCAGCGTGAACATTCT 480
QY 1070 GATATCATCTGATTTGTGATGCTCCGGGTGTTTCAACTAGAACTTTCAGACCAATGT 1129
DB 481 GATATCATCTGATTTGTGATGCTCCGGGTGTTTCAACTAGAACTTTCAGACCAATGT 540
QY 1130 TAGGAGAGAAATCTTTAAAGAAATTTGAGTGTGAGAGTTTGTCCAGAAATATCAGCTA 1189
DB 541 TAGGAGAGAAATCTTTAAAGAAATTTGAGTGTGAGAGTTTGTCCAGAAATATCAGCTA 600
QY 1190 GGGTACCTCAGAGATCAAGCTCAGTCTGTAACACATCCAGAAATTTTGTTCACGCA 1249
DB 601 GGGTACCTCAGAGATCAAGCTCAGTCTGTAACACATCCAGAAATTTTGTTCACGCA 660
QY 1250 TGTCAATTTCTCATATCTGATCTAGTACTTCTAGCTGTAGTTAGAGAAACAGCA 1309
DB 661 TGTCAATTTCTCATATCTGATCTAGTACTTCTAGCTGTAGTTAGAGAAACAGCA 720

QY 1310 TAAAGATGGAAGGAAACAGATGTTCTTATTTGCTTGTGGGCACTGTGATGAAGAA 1369
DB 721 TAAAGATGGAAGGAAACAGATGTTCTTATTTGCTTGTGGGCACTGTGATGAAGAA 780
QY 1370 GTCTTACAGTGTGGAAGAGGCTGCGAGAAACAGTGCACCCACTGATGATCAATTT 1429
DB 781 GTCTTACAGTGTGGAAGAGGCTGCGAGAAACAGTGCACCCACTGATGATCAATTT 840
QY 1430 GGGCAGAGAGTGTAGAAAGAAATAGAACCTTAAATATGCTCCCTTTGATGATCAAT 1489
DB 841 GGGCAGAGAGTGTAGAAAGAAATAGAACCTTAAATATGCTCCCTTTGATGATCAAT 900
QY 1490 GAGATCTCATGATTTCTACAGCCAGATGTTGCAAGTCTGTGATTCCTTCTTCC 1549
DB 901 GAGATCTCATGATTTCTACAGCCAGATGTTGCAAGTCTGTGATTCCTTCTTCC 960
QY 1550 TCAGAGCTGCACAGCAGCAACCGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1609
DB 961 TCAGAGCTGCACAGCAGCAACCGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1020
QY 1610 AAGAGCAATTTTAACTTACTATTTAGAACTCAGAAATCCCTGCTTACAAAG 1669
DB 1021 AAGAGCAATTTTAACTTACTATTTAGAACTCAGAAATCCCTGCTTACAAAG 1080
QY 1670 ATTATGCTGAGCCATGATTCAGGTGTTGGAATGGAATCTGTTGCTTATTTCTA 1729
DB 1081 ATTATGCTGAGCCATGATTCAGGTGTTGGAATGGAATCTGTTGCTTATTTCTA 1140
QY 1730 GAAATCTGAGTGTGAGAGATGAGTGGCTTCCAGGCTTCTTCCATGATGATGAGGCCC 1789
DB 1141 GAAATCTGAGTGTGAGAGATGAGTGGCTTCCAGGCTTCTTCCATGATGATGAGGCCC 1200
QY 1790 TGCTGTGGCAATTTGGGAGAGCACTGAAATTTCTGGGAGCAGAGTGAAGAGAGCCGA 1849
DB 1201 TGCTGTGGCAATTTGGGAGAGCACTGAAATTTCTGGGAGCAGAGTGAAGAGAGCCGA 1260
QY 1850 GTGGGGAGCCACAGTGGCTTCCAGCAGATCTCAGAGATGATGATGAGGAGAT 1909
DB 1261 GTGGGGAGCCACAGTGGCTTCCAGCAGATCTCAGAGATGATGATGAGGAGAT 1320
QY 1910 GCTGACAGCTTCTGTAAGTGTGTGCTGACCTGCTCAAGTGTAGTGTGCTTCT 1969
DB 1321 GCTGACAGCTTCTGTAAGTGTGTGCTGACCTGCTCAAGTGTAGTGTGCTTCT 1380
QY 1970 TAAAAACATTTAGAGGCTGCTGATATATCTCTTCCAGATTTAGCGGAAAGATCA 2029
DB 1381 TAAAAACATTTAGAGGCTGCTGATATATCTCTTCCAGATTTAGCGGAAAGATCA 1440
QY 2030 AACTTCAGAGACTTCTCCAGCCAGTGTGAGACACATCTAGTCAATTTGAGAGATCCA 2089
DB 1441 AACTTCAGAGACTTCTCCAGCCAGTGTGAGACACATCTAGTCAATTTGAGAGATCCA 1500
QY 2090 ATAGCCGACAGATGAGCTTCCATATACACATGTTGGAAGTGTGAAGGCGCAAGAG 2149
DB 1501 ATAGCCGACAGATGAGCTTCCATATACACATGTTGGAAGTGTGAAGGCGCAAGAG 1560
QY 2150 GAGAGTGGCAGTGTGCGAGAGAAATACTAAAGCTGATCTGATGATGATGATGATG 2209
DB 1561 GAGAGTGGCAGTGTGCGAGAGAAATACTAAAGCTGATCTGATGATGATGATGATGATG 1620
QY 2210 ATTATGCTTAAATTTGATTTCTTGGAAACCAATCAATCAATTTGCAAGAACTTC 2269
DB 1621 ATTATGCTTAAATTTGATTTCTTGGAAACCAATCAATCAATTTGCAAGAACTTC 1680
QY 2270 TTGGCGGCTTGTCTTATGATAGATGTTGTTGGAATTTCTGCTGATTTATTCCTC 2329
DB 1681 TTGGCGGCTTGTCTTATGATAGATGTTGTTGGAATTTCTGCTGATTTATTCCTC 1740
QY 2330 ATATGTCACTAGTATGATTTTCAAGCTGAGCTGTTGAAATCAGGTATTAAGCTGCG 2389
DB 1741 ATATGTCACTAGTATGATTTTCAAGCTGAGCTGTTGAAATCAGGTATTAAGCTGCG 1800
QY 2390 TGTCCTCTTAACCTTTGCTTTCAGATCTCATTTGATTAATTCCTCACTCAATGCTTGGCAAC 2449

Db 1801 TCTCCCTCTTAACCTTTTGGCTTGGCAATTCATTCAGCAATTTCCACCTGATGGTTGGCAAC 1860
Oy 2450 TTTCCAGAAAGATCTACTTGAAGTCTGCAAGATGGTTACTACAGTACCCATGTTGTTT 2509
Db 1861 TCTCTCGAGAGATATCTGAGCTCTGCGAGATGGTGAACCCAGTGCCTGGCTGTTT 1920
Oy 2510 CAAACCTGTAAATAATGCGAGTGTTCACAGTTCACACTACTCTACACAGAGATGCGTCCG 2569
Db 1921 CCAACCTGGTAACCATGTTAAATGCTTGTGCTCCACCCACTCTTACACAGATGCGCGGC 1980
Oy 2570 GTTGTATGGCTATTGACAGATGAGTGAATAATGGCGAAGCATTCAGTGGGCGTGAAG 2629
Db 1981 GTCGTATGGCTTCCCGGATGAGTGAATAATGGCGAGTCTTCCAGCTGGGTGGAG 2040
Oy 2630 ACATTTGGATGTCACAGAGACAGCTTTCAGAGCATCTGTCCCAACATATCTG 2689
Db 2041 ACAGTGGATGGCATCAGAGAG---CTTACAGCGCTGGCCCCCGAGCTGCT--- 2095
Oy 2690 AAACCAAGAGAAAGCTTCCCTGAGTGCACAGTCCATTTAAGAAACTGGAAAAAGAT 2749
Db 2096 -----AGAAAAAGCTCCCTTGAGCACACAGTCCATGAGAGAAAACTGGAAAAAGAC 2148
Oy 2750 TATGTCTACAAATTTAGTGGCAGTTCAGAGACATTTCTGAGAGACTGGCGACATTT 2809
Db 2149 TAAAGTCTACAGACTGAGTGGCAGCTGGAGAGACATTTCTACAGACTGGCGGCTCT 2208
Oy 2810 CAGTAGAGACTTCTAGTTTCACACACAAACAAACAAACAGAGAACAAAGCCAA 2869
Db 2209 CTGTAGAGACTTCCAGCT-----CAACAAACAGAGAAACAAACAGCCAG 2253
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Db 2254 CGGTCAAAACAAAGGCAACCCCAAGCTGAGTGTTCACACTCTCTTATCTCATC 2310
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Db 2311 ATGCTCAATTAATGTTTCCAGCAACATCAGCCCTTGTCTCTGCTGCTGCTGCTC 2367
Oy 2990 CTGGCAGTGCACAGATGTTCTTAAGCATAGACTTCAGGAGTTCATTCCTGTCAGAAATAC 3049
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Oy 3050 CTTGCTACCTCTGCAACAGCGCAGTTCCTTCTCAAAATTCACAGAAACTGCTCG 3109
Db 2416 CTTCCGACTCTCTGACACAGCGCAGTTCCTTCTCAAAATTCACAGAAACTGCTCG 2475
Oy 3110 AAAACAAAGACTCAGATAAATTTCCCAAGTCTTACTACAGTCAAGACCCCTGCTCCA 3169
Db 2476 AACACGAGACTCAGACACAGCTCTCCCAAGTCTTCACTCAGTCAAGACCCCACTCCA 2535
Oy 3170 GTACATACACAGCCCAAGCCATTAAGCTTACCCCAAGTAAATACAAAGTAAAGAGAG 3229
Db 2536 GTAAATACACAGCCCAAGCCATTCACACCCGTTCCGGGAGTACAAAGCAAACTAGGGG 2595
Oy 3230 ATCCCTCAAAAAATAGCATGACACTGATCTGAACAGTAGTTCCAAAATGTATGACAGT 3289
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Oy 3290 TTGGCTGACAGCAATAGTATGATGCTGTATACCCAGTACAGAGACAGAGTTCACCC 3349
Db 2656 TTGGGGGGGGGGGCAAGTGGCAACGCCGTATACCCAGCAGCAGACAGAGTTCACCC 2715
Oy 3330 CAGTAGAGAGAAATGACAGATTAATGATGCAATACAGAGCTCAACTCAGTATTTAGAGAC 3409
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Oy 3410 TTTCTGAAGCAATCTATGCTTCAACTGATACACAGTAACTTTTAAGTCAAGAGTGGCTG 3469
Db 2776 TTTCTGAAGCAATCTATGCTTCAACTGATACACAGTAACTTTTAAGTCCGAGCGCG 2835
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Db 2836 TCTCTCTCCGAAAAAGCCGAAATGACGACACTACAAAGCACAGCTCAATCATATTC 2895
Oy 3530 AAAAGTGCAAGAGAGATGGAAGCTGAAGAAAGAAAGACTTTAGCAATTTGCATGGCA 3589
Db 2896 AAAAGTGCAAGAGAGATGGAAGCTGAAGAGAGAGAGCTTTAGCATGCGCATGGCA 2955
Oy 3590 TGTCAAGCTCTCAGAGTATGCCCTCCCATAGTTCCTCAGTGCAGAGTTGAAAAATGGAAG 3649
Db 2956 TGTCAAGCTCTCAGAGTATGCCCTCCCATAGTTCCTCAGTGCAGAGTTGAAAAATGGAAG 3015
Oy 3650 ATATCATCTATTATTCACAGAGATACACGAGAGCTCTACAGAGATATACCAAGCAAAAC 3709
Db 3016 ATATTAATCTATCTACAGAGAGACACAGAAACTCTTCCAGGACATTCACCAAGCAAAAC 3075
Oy 3710 AACGTAATGAGAAAGACACTGATGAGTGAAGTGAAGTCAACAGATAGGCTTTGGAGCATTT 3769
Db 3076 AGCTTACAGAGAAAGAGCTGAGTGGCTGAAGGCGCAGAGATAGGCTTCGGAGCATTTT 3135
Oy 3770 CTTCTTTTATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTTTAAACAGTGA 3829
Db 3136 CTTCTTTTATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTTTAAACAGTGA 3195
Oy 3830 CTTATGTCAGAAACACATCTCTGAGCAAGAAAGTACTAGACACTAAGAGAAAGA 3889
Db 3196 CTTATGTCAGAAACACATCTCTGAGCAAGAAAGTACTAGACACTAAGAGAAAGA 3255
Oy 3890 TAAAGATGAGAGCACTGATCAATCAATCCAAACATTAATGATGTTGGAGCAGCTGTG 3949
Db 3256 TAAAGATGAGAGCACTGATCAATCAATCCAAACATTAATGATGTTGGAGCAGCTGTG 3315
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Db 3316 AGAAGAGCAATTAACATCTCTTCAATTAATGATGAGTGGAGGAGTGGCTCATTTGC 3375
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Db 3376 TGAGTAAATATGAGAGCTTCAAGATGAGTGAATGATTAATTAACACTGAAAGTAACTCC 3435
Oy 4070 GTGGCTTTCGTATCTCATGAAACCAAAATCTCACAGAGATGCAAAAGTGGCAATT 4129
Db 3436 GTGGCTTTCGTATCTCATGAAACCAAAATCTCACAGAGATGCAAAAGTGGCAATT 3495
Oy 4130 TGTCAATTAAGAGCACTGCTGACAGACTTAAGAAATTTGAGATTTGAGCTGACCCAGT 4189
Db 3496 TGTCAATTAAGAGCACTGCTGACAGACTTAAGAAATTTGAGATTTGAGCTGACCCAGT 3555
Oy 4190 TGGCATAAAGAGAACTGGTGCAGAGAGTTCAGAGACAAATTAATGGGAGCAATTTGAT 4249
Db 3556 TGGCATAAAGAGAACTGGTGCAGAGAGTTCAGAGACAAATTAATGGGAGCAATTTGAT 3615
Oy 4250 TTATGCACTGAGGTACTTAAGAGGTCAACAGTATGGAAGAGCTGTGATGATGAGGTG 4309
Db 3616 TCATGCGCGCTGAGGTCTTAAGAGGTCAACAGTATGATGATGATGATGAGGTG 3675
Oy 4310 TTGGCTGTGCTATTATGAATAATGGCTGTGCAAAAAACCACTAGGAATGCAAAAAACT 4369
Db 3676 TTGGCTGTGCTATTATGAATAATGGCTGTGCAAAAAACCACTAGGAATGCAAAAAACT 3735
Oy 4370 CCAATCATCTTCTTGAATTAATTAAGATTGTAAGTCACTGCTCATGATGCTCTT 4429
Db 3736 CCAATCATCTGCTTGAATTAATTAAGATTGTAAGTCACTGCTCATGATGCTCTT 3795
Oy 4430 CACATTTGTCTCTGTTTACAGAGATGTGGCTCTTCTGTTTAAAGTTCACCTCAGG 4489
Db 3796 CACATTTGTCTCTGTTTACAGAGATGTGGCTCTTCTGTTTAAAGTTCACCTCAGG 3855
Oy 4490 ACAGACCTTCATCAAGAGAGCTACAGAGATCCAGTCTTCTGCTACTACATGATG 4545
Db 3856 ACCGGCTTCGCTCAAGAGAGCTGTAACATCCGCTCTTCCGTACACAGTGGTAG 3911

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 3316 GCTGTATACCCAGTGAAGAGACAGTGTTCACCCAGTAGAGAGAAATGAGATATAGT 3375
 1275 GCCGTCATACCCAGGAGAGACAGTGTTCACCCAGTAGAGAGAAATGAGATATAGT 1334
 3376 GTCAATACAGAGCTCACTCCAGTATGAGACCTTCTTGAAGCATCTATGCTTCAAGT 3435
 1335 GTGACACCGAGCTCACTCCAGTATGAGACCTTCTTGAAGCATCTATGCTTCAAGT 1394
 3436 GATACAAAGTACTTTTAAAGTCAAGTGTGCTGCTCTCTGAAAAGGCTGAAAT 3495
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 1635 CCAGAGACTCTCTCCAGAGACATTCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1694
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 1695 CTGAAAGCTCAACAGATAGGCTTGGAGCATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1754
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 1755 GGAAGTGAAGCTTTAATGGCTGTAAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1814
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 3916 CCAAAATCATATAGATGTGGAGCCACAGTGTGAAGAGAGAGATATCAATCTCTTCAAT 3975
 1875 CCAAAATCATATAGATGTGGAGCCACAGTGTGAAGAGAGAGATATCAATCTCTTCAAT 1934
 3976 GAATGATGAGAGAGAGTGGTGGTGTGATGATGATGATGATGATGATGATGATGATGAT 4035
 1935 GATGATGATGAGAGAGAGTGGTGGTGTGATGATGATGATGATGATGATGATGATGATGAT 1994
 4036 TCAGTAGTATTAATCTACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 4095
 1995 TCAGTAGTATTAATCTACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2054
 4096 CAATATCATATGAGATGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGT 4155
 2055 CAGATCATATGAGATGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGT 2114
 4156 CTAAGAATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTT 4215
 2115 CTGAGAAATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTT 2174
 4216 GAGTTTCAGGGCAATTAATGAGGCAATTAATGAGGCAATTAATGAGGCAATTAATGAGG 4275
 2175 GAGTTTCAGGGCAATTAATGAGGCAATTAATGAGGCAATTAATGAGGCAATTAATGAGG 2234
 4276 CAACAGTATGAGAGAGCTGTGATGATGAGAGTGTGCTGTGCTGTGCTGTGCTGTGCT 4335
 2235 CAGCATGTATGAGAGAGCTGTGATGATGAGAGTGTGCTGTGCTGTGCTGTGCTGTGCT 2294
 4336 TGTGCAAAACCAACATGGAATGCAAAACCAACATGGAATGCAAAACCAACATGGAATG 4395

Db 2295 TGTGCAAAACCAACATGGAATGCAAAACCAACATGGAATGCAAAACCAACATGGAAT 2354
 4396 ATTGCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4455
 2355 ATTGCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2414
 4456 GTGGCTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4515
 2415 GTGGCTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2474
 4516 AAGCATCAAGTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4575
 2475 AAGCATCAAGTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2534
 4576 AAGCATCAAGTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4631
 2535 AAGCATCAAGTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2594
 4632 CCATGATGCTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4691
 2595 CCATGATGCTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2653
 4692 ATTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4750
 2654 ATTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4810
 4751 ACTGTAACCTGCTTCTCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4810
 2714 ACTGTAACCTGCTTCTCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2773
 4811 CATGACTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4864
 2774 CATGACTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2825

Db 2774 CATGACTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2825

RESULT 6
 US-08-472-934-1
 ; Sequence 1, Application US/08472934
 ; Patent No. 5753446
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHNSON, GARY L.
 ; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
 ; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,934
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/440,421
 ; FILING DATE: 15-May-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/354,516
 ; FILING DATE: 21-FEB-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 5,405,941
 ; FILING DATE: 15-Apr-1993
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/323,460
 ; FILING DATE: 14-Oct-1994
 ; PRIORITY APPLICATION DATA:

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APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. Decont, Jr. Esq.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: CPI-004DVCP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3260 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MEKK
STRAIN: murine
IMMEDIATE SOURCE:
LIBRARY: mouse liver
CLONE: MEKK cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..485
NAME/KEY: CDS
LOCATION: 486..2501
NAME/KEY: 3'UTR
LOCATION: 2502..3260
US-08-472-934-1

Query Match      37.3%; Score 1955.6; DB 1; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TAAACCTCTGACCACTGATGAGGAGAAAGATCAAACTTCAGAGACTTCACAGCCAGTT 2055
DB 1 TACACTCTCTGACCACTGAGGAGAGAAAGATCAAACTTCAGAGACTTCACAGCCAGTT 60
QY 2056 GTAGACACCATCTAGTCAATATGTCAGATGCCAATAGCCGACAGACTGCTCCATA 2115
DB 61 GTAGACACCATCTAGTCAATATGTCAGATGCCAATAGCCGACAGACTGCTCCATA 119
QY 2116 TCAACACTGTGGAACTGTGCAGAAAGCCAGAGAGAGAGTGGCAGTTGGCAGAGAAATA 2175
DB 120 TCTACAGTGTCTGAACTGTGCAGAAAGCCAGAGAGAGAGTGGCAGTTGGGAGAGAAATA 179
QY 2176 CTAAAGCTGATCCATCTGATATGATGATGATGATGATGATGATGATGATGATGATGAT 2255
DB 180 CTAAAGCTGATCCATCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 239
QY 2236 AACCAAACTGATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2295
DB 240 AACCAAACTGATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2299
QY 2296 CTGTGTGGAAATTTCTGTGTAATTTTATTCCTCATATTTGTCAGTACTGATGTTTCAAA 2355
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QY 2356 GCTGAGCTGTGTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2415
DB 360 GCTGAGCTGTGTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
QY 2416 TCCATGATATTTCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2475
DB 420 TCCATGATATTTCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
QY 2476 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2535

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DB 480 GCCAGATGGTGACCGAGTCCCGCTGTGTTCCTCAAGCTGGTGAACCATGTTAAAGCT 539
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RESULT 9

US-08-461-145C-1

Sequence 1, Application US/08461145C

Patent No. 6074861

GENERAL INFORMATION:

APPLICANT: JOHNSON, GARY L.

TITLE OF INVENTION: NOVEL MERK PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lathive and Cockfield, LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,145C

FILING DATE: 5-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/049,254

FILING DATE: 11-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/323,460

FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04178

FILING DATE: 15-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/354,516

FILING DATE: 21-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kara, Catherine J.

REGISTRATION NUMBER: P-41,106

REFERENCE/DOCKET NUMBER: CPI-004CNI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 3260 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MERK
STRAIN: murine
IMMEDIATE SOURCE:
LIBRARY: mouse liver
CLONE: MERK cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..485
NAME/KEY: CDS
LOCATION: 486..2501
NAME/KEY: 3'UTR
LOCATION: 2502..3260
US-08-461-145C-1

Query Match 37.3%; Score 1955.6; DB 3; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

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DB 61 GTAGACACCATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 119
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RESULT 10
US-08-628-829-1
; Sequence 1, Application US/0862829A
; Patent No. 6333170
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External
; FILE REFERENCE: CPI-004DVP3
; CURRENT APPLICATION NUMBER: US/08/628,829A
; EARLIER FILING DATE: 1996-04-05
; EARLIER APPLICATION NUMBER: 08/440,421
; EARLIER FILING DATE: 1995-05-15
; EARLIER APPLICATION NUMBER: 08/323,460
; EARLIER FILING DATE: 1994-10-14
; EARLIER APPLICATION NUMBER: 08/049,254
; EARLIER FILING DATE: 1993-05-15
; EARLIER APPLICATION NUMBER: 08/410,602
; EARLIER FILING DATE: 1995-04-24
; EARLIER APPLICATION NUMBER: 08/472,934
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3260
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (486)..(2501)
; US-08-628-829-1

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Query Match      37.3%; Score 1955.6; DB 4; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

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Db	2115	CTGAGAAATTCGACACTTTTGGAGCTGCTGCCAGTTTGATCAAAAGAGAACCGGTACAGGA	2174
Qy	4216	GAGTTTCAGGAGCAATTAATCTGGGGACAAATTTGCAATTTATGGAACCTGAGGTACTAAGAGT	4275
Db	2175	GAGTTTCAGGAGCAAGTTACTGGGGACAAATTTGCAATTCATGAGCGCTGAGGTCTTAAGAGT	2234
Qy	4276	CACACGATATGGAAGGAGCTGTGATGTATGAGAGTGTGGCTGTGCTATTTATAGAAATGGCT	4333
Db	2235	CAGACGATATGATGAGGAGCTGTGATGTATGAGAGTGTGGCTGTGCTATTTATAGAAATGGCT	2294
Qy	4336	TGTGCAAAACACCATATGGAATGTGAGAAACAACTCCAAATCATCTGCTTGTGATTTAAG	4395
Db	2295	TGTGCAAAACACCTTGTGAATGTGAGAAACAACTCCAAATCATCTGCTTGTGATTTAAG	2354
Qy	4396	ATTGCTATGATCACTACTGCTCCATCGATGATCCCTTCACTATTTGCTCTCTGTTACGAGAT	4455
Db	2355	ATTGCTATGCGCACTACTGCACTGCACTCATCTCCGCTACACCTGTCCCGGGGTGTGGCGAC	2414
Qy	4456	GTGGCTCTTGTTGTTTATGAACTTCAACTCTCAGGACAGACCTTCATCAAGAGAGCTACTG	4515
Db	2415	GTGGCTCTTGCGCTGTGATGAACTTCAAGCCTCAAGACACCGGCTCTCCGCCAGAGAGCTGCTG	2474
Qy	4516	AAGATCCAGCTCTTGTCTACTACTAGATGGTATGCCAATTAATGACATCAACATCACTGTAAGAC	4575
Db	2475	AACATCCCGGCTCTTGTCTACTACAGTGGTATTAATGTTCAAGTCAAGCTCTATGAGAGAC	2534
Qy	4576	AGATATGCTCAACAAGAAAAAAACCTTGC---TGGGAGAACACAAATTCATTTACTACTGG	4633
Db	2535	AGATATTCGAACCGGAGAGAGAAAAAGAACATTTGTTGGGCGACACATGCCGCTTAACCGCAG	2594
Qy	4632	CCATGATGCCATGACAGCTATGAACGAGGCCAGTGGGAAACCTTATCTTAAGTATGG	4691
Db	2595	CCCTACAGCCACTGTAACAGCCAGAAACGGGGCCAGCGGGGAAA--CGCTACCTTAACGATGAG	2653
Qy	4692	ATTGACAAATCATGATGTATACCTTAAGGATCAAGATCAAGTCA--AAAGCCCAAACTGTGACAGA	4755
Db	2654	ATTGACAAATCATATGATCTGTATGATGAAGTGTGATGTCAAGACATCTACACTGTGTCAGGA	2713

QY	4751	ACTTAAACGTGGCTTTCAAAGAAACGTGGCCCTAGTGAACAGAAACCAATGAAGTTTG	4810
Db	2714	ACTGCACACCGTGGCTTTCACAGACTGGCTGCGGGGACACAGAAAGCGATGAGTTTG	2773
QY	4811	CATGACCAAAATTCAGAAAGATAAATTTATTTTTCGAGGACCTTTTCAGCA	4864
Db	2774	CATACCAAGAAAGAAAGCATTAATTTTA--TTTTCGAGGACCTTTTCAGCTA	2825

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US-08-472-934-11
: Sequence 11 Application US/08472934
: Patent No. 575346
:
: GENERAL INFORMATION:
: APPLICANT: JOHNSON, GARY L.
: TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
: TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lohive and Cockfield
: STREET: 60 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02109
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/472,934
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/440,421
: FILING DATE: 15-MAY-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/354,516
: FILING DATE: 21-FEB-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 5,405,941
: FILING DATE: 15-APR-1993
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/323,460
: FILING DATE: 14-OCT-1994
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/11690
: FILING DATE: 14-OCT-1994
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/04178
: FILING DATE: 15-APR-1994
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Giulio A. DeConti, Jr. Esq.
: REGISTRATION NUMBER: 31,503
: REFERENCE/DOCKET NUMBER: CPI-004DVC2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2503 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 466..2325
: US-08-472-934-11

```

Best Local Similarity 48.2%; Pred. No. 2.1e-08;
Matches 336; Conservative 0; Mismatches 352; Indels 9; Gaps 4;

OY 3666 ACAGATACACGAGAGACTCTACCAAGACATACCAAAAGCAAAACCTATAGAGAGA 3725
DB 1464 AGACAACTCTACTTGTAGCTGACAGACATCAAGCCACCCAGCTCAGCTCGAGCTCC 1523
OY 3726 CACTGATGCTGAAAGGTCAACAGATAGCCCTTGAGAGCAATTTCTTCTTATCAGGC 3785
DB 1524 GACCAACTGAGACACTGAGCAAGCTCTTGCCAGAGAGCTTTGGTAGGGCTACTCTG 1583
OY 3786 TCAAGATGGGAGACTGAGCACTTATAGCTTAAACAGGAGCTTATGTCAGAAAC 3845
DB 1584 CTATGATGTTGATACCGGAGAGAGCTGCTTTAAAGCAATTTAGCTTAAACCTGAGG 1643
OY 3846 ATCTTCTGAGCAAGAAAGATAGTAAAGCACTAAGAGAGAAATTAAGATGAGCA 3905
DB 1644 CCCAGAGACCAAGAGAAAGTAAATGCACTTATGATGTGAATTCAGTTTGAAGAACTT 1703
OY 3906 TCTGAATCATCCAA-ACATCATTTAGAGATTGGGAGCCAGCTGTGAGAAAGCAATTACA 3964
DB 1704 GTTGATGAGCAATTTGCTACATTTATGCTGTTGAGGAGATCCCTCAGAGAAAAACT 1763
OY 3965 ATC--TCTTCATTTGAATGATGAGGAGGAGTCCGCTCATTTGCTGATTAATATG 4022
DB 1764 TTCCATCTTTATGAGATATATCCAGGGGTTCAATTAAAGCACTAAAGCCTACGG 1823
OY 4023 AGCTTCAAGAAATAGTATTAATTAACACTGACAGTACCTGAGCTTTCGTA 4082
DB 1824 AGCTTCTTATGAGAGCTGACAGAGAGTACACCGCTGATTTGAGAGGGGCTCATTA 1883
OY 4083 TCTCATGAAAAACAATCATTCACAGAGATGTCAAGAGTGGCAATTTCTTAATGACAG 4142
DB 1884 TTTGATAGTAAATATGATTTGCTCAGATATCAAGAGCAAAATATCTTAAGGATTC 1943
OY 4143 CACTGTGAGACTAAGATTAAGATTTGAGACTGAGCAGTGGCTGCAAAAG 4202
DB 1944 CACAGGCAATATC--AAGTTAGAGACTTTGGGCTAGTAAAGGCTTACAGACCTGT 2001
OY 4203 AACTGTGAGAGAGATTTCAAGGACAAATTACTGGGACAAATTTGATTTGGCACTGA 4262
DB 2002 CTCTAGGAGACAGAAAT---GAGTCTGTACAGGACAGCACTACTGATAGTCTGA 2057
OY 4263 GGTACTAAGAGTCAACAGTATGAGAGAGCTGTGATGATGAGTGTGGCTGTACT 4322
DB 2058 GGTCTATCTGAGAGAGGATGAGAAAGCAAGCAATCTAGTGTAGCATGTACTGT 2117
OY 4323 TATGAATGCTGTGCAAAACCAACATGSAATGCA 4359
DB 2118 GGTAAATGCTAATGTAAGAAAGCACTTTGGGCTGAA 2154

RESULT 12
US-08-461-146C-11
Sequence 11, Application US/08461146C
Patent No. 5981265
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHODS FOR REGULATING MEK PROTEIN ACTIVITY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahlive and Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461.146C
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPT-004CN3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 466..2325
US-08-461-146C-11

Query Match 1.4%; Score 75.8; DB 2; Length 2503;
Best Local Similarity 48.2%; Pred. No. 2.1e-08;
Matches 336; Conservative 0; Mismatches 352; Indels 9; Gaps 4;

OY 3666 ACAGATACACGAGAGACTCTACCAAGACATACCAAAAGCAAAACCTATAGAGAGA 3725
DB 1464 AGACAACTCTACTTGTAGCTGACAGACATCAAGCCACCCAGCTCAGCTCGAGCTCC 1523
OY 3726 CACTGATGCTGAAAGGTCAACAGATAGCCCTTGAGAGCAATTTCTTCTTATCAGGC 3785
DB 1524 GACCAACTGAGACACTGAGCAAGCTCTTGCCAGAGAGCTTTGGTAGGGCTACTCTG 1583
OY 3786 TCAAGATGCTGGAAGTCAACTTTAATGCTTTAAACAGGTGACTTATGTCAGAAAC 3845
DB 1584 CTATGATGTTGATACCGGAGAGAGCTGCTGTAAAGCAAGTTCAAGTTCAGCTGAGG 1643
OY 3846 ATCTTCTGAGCAAGAAAGTATGTAAGCACTAAGAGAGAAATTAAGATGAGCA 3905
DB 1644 CCCAGAGACCAAGAGAAAGTAAATGCACTTATGATGTGAATTTCAAGTGTAAAAACTT 1703
OY 3906 TCTGAATCATCCAA-ACATCATTTAGAGATTGGGAGCCAGCTGTGAGAAAGCAATTACA 3964
DB 1704 GTTGATGAGCAATTTGCTACATTTATGCTGTTGAGGAGATCCCTCAGAGAAAAACTT 1763
OY 3965 ATC--TCTTCATTTGAATGATGAGGAGGAGTCCGCTCATTTGCTGATTAATATG 4022
DB 1764 TTCCATCTTTATGAGATATATCCAGGGGTTCAATTAAAGCACTAAAGCCTACGG 1823
OY 4023 AGCTTCAAGAAATAGTATTAATTAACACTGACAGTACCTGAGCTTTCGTA 4082
DB 1824 AGCTTCTTATGAGAGCTGACAGAGAGTACCCGCTGATTTCTGAGAGGGGCTCATTA 1883
OY 4083 TCTCATGAAAAACAATCATTCACAGAGATGTCAAGAGTGGCAATTTCTTAATGACAG 4142
DB 1884 TTTGATAGTAAATATGATTTGCTCAGATATCAAGAGCAAAATATCTTAAGGATTC 1943

EARLIER APPLICATION NUMBER: 08/472,934
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 2503
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (466)..(2322)
US-08-628-829-7

Query Match 1.4%; Score 75.8; DB 4; Length 2503;
Best Local Similarity 48.2%; Pred. No. 2.1e-08;
Matches 336; Conservative 0; Mismatches 352; Indels 9; Gaps 4;

QY 3666 ACAGGATACACGAGACTCTACACGAGACATTCACCAACCAACCAACCGTATAGACAGCA 3725
DB 1464 AGACATCTCTACTTTGACTCTCAGACATCAGCCACCACCGTTCACCTGAGCTCC 1523
QY 3726 CACTGATGGCTGGAAGGTCAACAGATAGCCCTTGAGCATTTCTCTGTTATCAGGC 3785
DB 1524 GACCAACTGGAGACTGGGCAAGCTCTGCGCAAGAGCTTTGGTAGGCTTACTCTG 1583
QY 3786 TCAGATTTGGAGACTGCACTTTAATGGCTTTAAACAGCTGACTTATGTCAGAACAC 3845
DB 1584 CTATATGTTGTTATACCGAAGAGAGCTGCTTTAAGCAAGTTCACTTAACCTGAGAG 1643
QY 3846 ATCTTCTGAGCAAGAGAGTAGTAGAAGCACTAAGAGAGATTAAGATATAGACCA 3905
DB 1644 CCCAGAGCCAGCAAGAGAGATTAATGACCTGAGTGTGAATTCAGTTGTTAAACTT 1703
QY 3906 TCTGATATCCCA-ACATCATTTAGATGTTGGAGCCACGCTGAGAGCAATTTACA 3964
DB 1704 GTTGATGAGGCAATTTGTTGATTTATGAGGCTTTGAGGAGTCCCTGAGCAAAACT 1763
QY 3965 ATC--TCTTCAATTTGATGATGAGGAGGATCGTGGCTCATTTGCTGAGTAAATATGC 4022
DB 1764 TTCCATCTTTATGAGTATGATGAGGAGGCTTCAATTAAGCACTAAAGCCTACGG 1823
QY 4023 AGCCCTCAAGATCAGTATTAATTAACATCAACATGACATTAACCTGCGCTTCCGA 4082
DB 1824 AGCTTCTCTGGAAGAGGAGAGAGATACCCGTCAGATTTGAGAGGGGCTCCATTA 1883
QY 4083 TCTCATGAAAAACCAATCATTTACAGAGATGTCAAAGGTGGCAATTTGCTAATTTAGACAG 4142
DB 1884 TTTGATATGTAATATGATTTGTCATAGATATCAAGAGCAATTTATCTTAAGGGATTTC 1943
QY 4143 CACTGCTCAGAGACTTAAGATTTGCAATTTGAGCTGCAGCCAGGCTTGCATCAAAAGC 4202
DB 1944 CACAGGCAATATC--TAGTTAGGAGACTTTGGGCTAGTAAAGGCTTCAGACCATCTGT 2001
QY 4203 AACGTCGAGAGAGTTTACGGGCAATTAACCTGGGCAATTTGATTTATGAGCCATGA 4262
DB 2002 CTCTGAGGCAACGCAAT-----GAAGTGTCTACAGGACAGCCCATCTGAGATGCTGA 2057
QY 4263 GGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGATGAGTGTGGCTGTAT 4322
DB 2058 GGTATCATGTGGAGAGGCTATGGAAGAAAGCAGACATCTGAGTGAAGCATGTACTGT 2117
QY 4323 TATGAATATGCTTGCAGAAACCAACCATGCAATGCA 4359
DB 2118 GGTAGAAATGCTAACTGAAAGCCACCTTGGGCTGAA 2154

RESULT 15
US-09-359-757-1
Sequence 1, Application US/09359757
Patent No. 6080546
GENERAL INFORMATION:
APPLICANT: Brett P. Montia
APPLICANT: William Gaarde

APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF MEK5 EXPRESSION
FILE REFERENCE: RTS-0078
CURRENT APPLICATION NUMBER: US/09/359,757
CURRENT FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 5236
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (361)..(4485)
FEATURE:
NAME/KEY: unsure
LOCATION: 4687
OTHER INFORMATION: unknown
US-09-359-757-1

Query Match 1.4%; Score 74.4; DB 3; Length 5236;
Best Local Similarity 50.4%; Pred. No. 6.6e-08;
Matches 245; Conservative 0; Mismatches 226; Indels 15; Gaps 2;

QY 3883 GAAGAGATTAAGATATGAGCCATCTGAATCATCCAAACATCATTAAGATGTTGGAGCC 3942
DB 2530 GAAGAAATAGCATTCATTAACACCTGAAGCAAAATAATGTCAGTATCTGGGCTCT 2589
QY 3943 ACGTGGAGAGAGCAATTAACATCTTCAATGATGATGAGGAGATCGGTGGCT 4002
DB 2590 TTCACTGAGAAATGTTTATTAATCTTCATGAGAGCCAGTCCCTGAGAGAGTCTTCT 2649
QY 4003 CATTTGCTGAGTAAATATG-----AGCTTCAAGAAATCAGTATTAATTAATAC 4053
DB 2650 GCTCTCTCTGTTCAAAATGGGCTCATTAAGACATTAAGCAAAATGAGTGGCTTTAT 2709
QY 4054 ACTGAACATTAATCTGCGGCTTTCGATGTCCTGATGAAACCAATATTCACAGACAT 4113
DB 2710 ACAAAGCAATTAATCTGGAAGATTAATAATATCTCCATGACCAATCAGATAGTTCACCGGAGC 2769
QY 4114 GTCNAAGTGGCAATTTGCTAATTTGACAGCACTGCTCAGAGACTAAGATGACAGATTT 4173
DB 2770 ATAAAGGTGACAAATGTTGATTAATTAATCTTAACATGAGTGTCTCAATCTCTGACTTC 2829
QY 4174 GGAGCTGACCCAGGTTGGCATCAAAAGCAATGCTGAGAGAGATTTCAAGGACAAATTA 4233
DB 2830 GGAACATCAAAAGAGGCTTGCTGATTAACCCCTGACTGAATTTACTGTACCTTC 2889
QY 4234 CTGGGAGCAATTTGCTTTATGACCTGAGGTACTTAAGAGTCAACACATATGGAAGAGC 4293
DB 2890 CAGTATATGGCACCAGAAATTAATAGATAAGGACCAAGAG-----CTACGGAAGAGCA 2943
QY 4294 TGTGATGATGAGAGTGTGGCTGCTATTAATGAAATGGCTTGTGCAAAACCATATGG 4353
DB 2944 GCAGCATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3003
QY 4354 AATGCA 4359
DB 3004 TATGAA 3009

Search completed: December 27, 2002, 22:19:40
Job time : 303 secs